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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score 319 319 319 317 Query Match Length BB NEXITS AE7184406 AF150466 AF150467 AF17840567 AF178407 AF178401 AF178407 AF178408 AE7178408 AE7178408 AE7178418 AE7178416 AF178416 AF178416 AF178416 AF178404 AF178416 AR206400 AR206400 BD083591 AF117921 AY429048 AY429053 AY3104429049 AY429049 AY429049 AF178394 AF178401 AF178397 AF178397 AF178397 AF178413 AF178413 AF178413 AF178412 NHA317959 ij ALIGNMENTS AF178404 Fusarium AF130142 Nectria h AF437761 Fungal is AF178410 Nectria hae AF178421 Nectria hae AF178421 Nectria h AY332483 Stenocarp AY188918 Nectria h AY332486 Stenocarp AF178399 Fusarium AY273332 Unculture AF15451 Nectria h AF455451 Nectria h AF178394 Nectria h AF178401 Nectria h AF178401 Nectria h AF178401 Nectria h AF178402 Fusarium AF178402 Fusarium AF178402 Fusarium AF178402 Fusarium AF178406 Nectria h L36627 Neccosmos AJ317959 Nectria h AF150466 Nectria h AF150466 Nectria h AF150467 Nectria h AF178407 Fusarium AF178408 Fusarium AF178408 Fusarium AF178409 Fusarium AF178409 Fusarium AF178416 Nectria h AY310442 AY429049 AY429048 AY429053 AR206400 Description Chaetomiu Chaetomiu Nectria h Chaetomiu Sequence Nucleic a

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AR206400	RESULT 1
filamentous tungi Patent: US 6372430-A 6 16-APR-2002;	Nucleic acids for detecting Aspergillus species and other	Morrison, C.J., Reiss, E., Aidorevich, L. and Choi, J. Soo.	1 (bases 1 to 319)	Unclassified.	Unknown.	Unknown.		AR206400.1 GI:21504990	AR206400	Sequence 6 from patent US 6372430.	AR206400 319 bp DNA linear PAT 20-JUN-2002		

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Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

2E 1 (bases 1 to 319)
Nucleic acids for detecting Aspergillus species and other
filamentous fungi
AL Patent: JP 2001525665-A 6 11-DEC-2001;
THE GOURENMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O
CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND
PREVENTION TECHNOLOGY TRANSFER OFFICE
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/organism="Fusarium solani"
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/db_xref="taxon:169388"
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                                                                                                                                                                                                                                                                                                  Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998) 2 (bases 1 to 319) Choi,J.S., Westerman,J.M. and Morrison,C.J. Direct Submission Direct Submission Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF117921 319 bp DNA linear PLN 17-JUN-2000 Nectria haematococca 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

RNA gene, partial sequence.

AF117921
AF117921.1 GI:8570107
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 319)
Choi, J.S., Westerman, J.M. and Morrison, C.J.
Rapid differentiation of filamentous fungi using species-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H
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100.0%; Score 319; DB 8; llarity 100.0%; Pred. No. 1.4e-79; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                             /organism="Fusarium solani"
/mol_type="genomic DNA"
/db_xref="taxon:169388"
                                                                                                                 /product="internal transcribed note="ITS2"
                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                    product="28S
                                                                                                                                                    /product="5.8S ribosomal RNA"
L60. .272
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Pred. No. 1.4e-79;
, Mismatches 0;
                                                                                    ribosomal RNA"
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                               Length 319;
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                       63
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Submitted (07-OCT-2003) Division
Road, New Delhi, Delhi 110012, Ir
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Chaetomium globosum
Chaetomium globosum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
                                                                                                                                                                                                                                                                                                                                                 Aggarwal,R., Renu,S. and Singh,D.V.
Nucleotide sequence of full length ITS
Chaetomium globosum
                                                                                                                                                                                                                                                                                                              2 (bases 1 to 559)
Aggarwal,R., Renu,S. and Singh,D.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY429048.1 GI:38503524
                                                                                                          Similarity
                                                           AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTTGAACGCACA 62
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                      TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGCC 122
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                                                                                              Conservative
                                                                                                                                                       /note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed space 2, and 28S ribosomal RNA"
                                                                                                                                                                                                   /db_xref="taxon:38033"
                                                                                                                                                                                                                   organism="Chaetomium globosum"
/mol_type="genomic DNA"
/isolate="Cg1"
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                                                                                      99.4%; but
100.0%; Pre
                                                                                          Score 317; DB 8; L
Pred. No. 5.4e-79;
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Best Local Similarity
Matches 317; Conserv
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Chaetomium globosum
Chaetomium globosum
Chaetomium globosum
Bukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Bukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Chaetomium.

1 (bases 1 to 561)
Aggarwal,R., Renu,S. and Singh,D.V.
Nucleotide sequence of full length ITS region of Cg6 isolate of Chaetomium globosum
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Road, New Delhi, Delhi 110012, India
Location/Qualifiers
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AY429053
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TACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAGA
                                                                                                               CCCGGGCCTGGCGTTGGGGGATCGGCGGAAGCCCCCTGCGGGGCACAAAACGCCGCTCCCCCAAA
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                                                                               CCCGGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="contains 18S ribosomal
spacer 1, 5.8S ribosomal RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Chaetomium globosum"
/mol_type="genomic DNA"
/isolate="Cg6"
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Pred. No. 5.4e-79;
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Direct Submission

Submitted (02-JUN-2003) Agronomy and Horticulture, Submitted (02-JUN-2003) Agronomy and Horticulture, Of Queensland, Warrego Highway, Gatton, QLD 4343, 1

of Queensland, Warrego Highway, Gatton, QLD 4343, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 576)
Scott, P.T., Martin, H.L., Boreel, S.M., Wearing, A.H. and Maclean, D.J. Isolation and characterization of Nectria haematococca from table beet grown in the Lockyer Valley, Queensland, Australia
                                                                                                                                                                                                                                                                                                                                      Similarity
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GCGGCGCGCCACGCCGTAAAACACCCAACTTCTGAATGTTGACCTCGAATCAGGTAGGA
                                                   TACAGTGGCGGTCCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Nectria haematococca"
|mol_type="genomic DNA"
|db_xref="taxon:140110"
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Pred. No. 5.4e-79;
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Nucleotide sequence of full-length ITS region
Chaetomium globosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (07-OCT-2003) Division of
Road, New Delhi, Delhi 110012, India
Location/Qualifiers
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Chaetomium globosum
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Chaetomiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AY429049 569 bp DNA linear PLN 30-NOV-20 Chaetomium globosum isolate Cg2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S
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Aggarwal,R., Renu,S
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AY429049.1 GI:38503525
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                                                                      ATACCCGCTGAACTTAA 319
                                                ATACCCGCTGAACTTAA 528
                                                                                                                                  GCGGCGCGCCACGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGGA
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spacer 1, 5.8S ribosomal RNA,
2, and 28S ribosomal RNA"
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/isolate="Cg2"
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/mol_type="genomic DNA"
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Pred. No. 1.5e-78;
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Eukaryota; Fungi; Ascomycota; environmental samples.
1 (bases 1 to 501)
Roose-Amsaleg,C., Brygoo,Y. and Harry,M.
Marked discrepancy between fungal diversity in soil-feeding termitaries and tropical soils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-APR-2003) UFR Sciences Universite Paris 12, UMR137-LBSE, Avenue du General de Gaulle, Creteil cedex 94010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   France
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                                                                                                                                    CCCGGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTGCGGGGCACAAGCGCCGTCCCCCAAA 182
                                                                           GCGGCGCGCCACGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGGA 302
                                                                                                                                                                                                                                                         TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGCC
                                                                                                                                                                                                                                                                                                  AMATIGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
                                                                                                                                                                                                                                                                                                                   AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
                         ATACCCGCTGAACT 316
                                                                                                                                                                             CCCGGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTGTGGGCGCAACGCCGTCCCCCAAA
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                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="uncultured ascomycete"
/mol type="genomic DNA"
/isolation_source="termitarie of Cubitermes
dominated by Aucoumea klaineana)"
/db_xref="taxon:175243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="5.8S ribosomal
293. .>501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="contains 18S ribosomal RNA
spacer 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains internal transcribed
ribosomal RNA"
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/country="Gabon: Doda, La Lope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="T7A6"
                                                                                                                                                                                                                                                                                                                                                                            96.9%;
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                                                                                                                                                                                                                                                                                                                                                             Score 309.2; DB 8;
Pred. No. 8.7e-77;
0; Mismatches 3;
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RESULT

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2 (Dases 1 to 509)

Iwen,P.C., Henry,T. and Hinrichs,S.H.

Direct Submission

Submitted (07-JUL-1999) Pathology and Microbiology, University of Submitted (07-JUL-1999) Pathology and Medical Center, Omaha, NF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 509)

Iwen, P.C., Henry, T. and Hinrichs, S.H.
Sequence analysis of the internal transcribed spacer regions of Fusarium species most commonly associated with human invasive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF165874 509 bp DNA linear PLN 18-JUL-199: Nectria haematococca internal transcribed spacer 1, 5.85 ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 285 ribosomal RNA gene, partial sequence.
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                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                    ATACCCGC 310
                                                         GCGGCGCGCCACGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGGA
                                                                               GCGGCGCGGCCACGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGGA
                                                                                                                                           CCCGGGCCTGGCGTTGGGGGATCGGCGGAAAGCCCCCTGCGGGCACAACGCCGTCCCCAAA
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/product="28S ribosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="ITS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="internal transcribed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:169388"
note="anamorph: Fusarium solani"
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strain="ATCC62877"
                                                                                                                                                                                                                                                                                                                                                                        96.6%;
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                                                                                                                                                                                                                                                                                                                                                                      Score 308; DB 8;
Pred. No. 1.9e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission Submitted (04-DEC-2001) Laboratory for Mycology and Molecular Submitted (14-DEC-2001) Laboratory for Mycology and Molecular Biology, ENT-University Hospital, Auenbruggerplatz 26-28, Gra-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreamycetidae; Hypocreales; Nectriaceae; Nectria.
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Med. Mycol. 41 (2), 149-161 (2003)

2 (bases 1 to 582)

Buzina, W., Braun, H., Freudenschuss, K., Lack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 582)
Buzina,W., Braun,H., Freudenschuss,K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                     ATACCCGCTGAACTTAA 319
                                                                                      GCGGCGCGCCACGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGGA
                                                                                                                                      TACAGTGGCGGTCCCGCCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAGA
                                                                                                                                                        TACAGTGGCGGTCCCCGCCGCAGCTTCCATTGCGTAGCTAACACCCTCGCAACTGGAGA
                                                                                                                                                                                                                             CCCGGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCCAAA
                                                                                                                                                                                                                                                                       TTGCGCCCGCCAGTATTCTGGCGGCCATGCCTGTTCGAGCGTCATTACAACCCTCAGGCC
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ATACCCGCTGAACTTAA
                                                                     GCGGCGCGCCATGCCGTAAAACACCCAACTTCTGAATGTTGACCTCGAATCAGGTAGGA
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353. .524
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525. .>582
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/mol_type="genomic DNA"
/isolate="wb394"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="large subunit ribosomal
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Pred. No. 3.1e-74;
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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RESULT 12 AF178401

DEFINITION Locus

AP178401 PLN 20-DEC-200 NA linear PLN 20-DEC-200 Nectria haematococca mpIV strain NRRL22277 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28

PLN 20-DEC-2001

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AUTHORS
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AUTHORS
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Best Local S
Matches 312
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordari.
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
1 (bases 1 to 550)
O'Donnell,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF178394 550 bp DNA linear PLN 20-DEC-200 Nectrial haematococca mpIV strain NRLL22163 185 ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.85 ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28 ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (18-AUG-1999) Microbial Properties Research, Submitted (18-AUG-1999) Microbial Properties Research, ARS, 1815 N. University St., Peoria, IL 61604, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                         GCGGCGCGCCACGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGGA
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                                                                                                         TACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAGA
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/note="forma specialis: xanthoxyli; anamorph: Fusarium solani f. sp. xanthoxyli"
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2, and 28S ribosomal RNA"
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spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
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                                                  Nectria haematococca 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
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Fusarium
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                                         AF129104.1 GI:4512119
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spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, and 28S ribosomal RNA"
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/mol_type="genomic DNA"
/strain="NRRL22277"
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             Eukaryota; Fungi; Ascomycota; Pe
Hypocreomycetidae; Hypocreales;
1 (Dases 1 to 548)
O'Donnell,K.
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2 (bases 1 to 548)
O'Donnell,K.
                                                                                                                                                                                                                                                                             AF178398 549 bp DNA linear PLN 20-DBC-20 Nectria ipomoeae strain NRFL22101 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
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Submitted (18-AUG-1999) Microbial Properties Research, NCAUR, USDA,
ARS, 1815 N. University St., Peoria, IL 61604, USA
                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Nectriaceae; 1 (bases 1 to 549) O'Donnell, K.
                                                                                             2 (bases 1 to 549)
O'Donnell, K.
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                                                                                                                                      Molecular phylogeny of the
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Nectria ipomoeae
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spacer 1, 5.8S ribosomal RNA,
2, and 28S ribosomal RNA"
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/organism="Nectria ipomoeae"
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/db_xref="taxon:57162"
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
127.4	127.8	128.4	131.8	133.4	134.2	138.8	138.8	145.6	154.8	155	156.8	163.6	165.2	165.2	165.2	165.2	165.2	166.8	171.4	174.8	174.8
39.9	40.1	40.3	41.3	41.8	42.1	43.5	43.5	45.6	48.5	48.6	49.2	51.3	51.8	51.8	51.8	51.8		52.3	53.7	54.8	54.8
537	553	605	652	686	382	549	549	809	545	537	610	615	667	664	632	632	625	659	504	503	503
9	w	N	7	9	ω	w	w	N	Ŋ	w	N	σ	σ	σ	σ	σ	σ	თ	4	N	N
ABA01153	AAZ91726	AAX90108	ABZ20765	ABV78727	AAA72783	AAZ91724	AAZ91723	AAX90110	AAT05403	AAZ91725	AAX90111	AAF76260	ABV78712	ABV78703	ABV78706	ABV78709	ABV78718	ABV78715	AAS08426	AAV59029	AAV62592
Aba01153 Deuteromy	Aaz91726 Rosellini	Aax90108 Eutypella	Abz20765 Muscodor		Aaa72783 5.8s rRNA	Aaz91724 Rosellini	Aaz91723 Rosellini	Aax90110 Phomopsis	Aat05403 Microdoch	Aaz91725 Rosellini	Aax90111 Phomopsis	Aaf76260 Cordyceps	Abv78712 C. sinens	Abv78703 C. sinens	Abv78706 C. sinens	Abv78709 C. sinens	Abv78718 C. sinens	Abv78715 C. sinens	Aas08426 Internal	Aav59029 F. gramin	Aav62592 Fusarium

ALIGNMENTS

RESULT 1 AAV70850 ID AAV70850 E

standard; DNA;

319

₽₽

AAV70850;

26-FEB-1999

(first entry)

Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger;
A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii;

Internal transcribed spacer 2 (ITS2) and adjacent regions.

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The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species-specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. funigatus; M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus; R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
                                                                                                                                               New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothr
                                                                                                                                                                                                                                                                                                               02-MAY-1997;
                                                                                                 Claim 1; Page 12; 45pp; English.
                                                                                                                                                                                                                WPI; 1999-034737/03.
                                                                                                                                                                                                                                                Morrison CJ,
                                                                                                                                                                                                                                                                                                                                                01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusarium solani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penicillium notatum; Sporothrix schenkii;
                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                              Reiss E,
                                                                                                                                                                                                                                                                                                                 97US-0045400P.
                                                                                                                                                                                                                                                                                                                                                98WO-US008926.
                                                                                                                                                                                                                                                Aidorevich L, Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              filamentous fungus; ss
                                                                                                                                                 Sporothrix
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ARSIGET 2
AAS16211
ID 1821
AX AAS1
XX AAS1
XX AAS1
XX Gibb
XX Gibb
XX Flow
XX Flow
XX Flow
XX Gibb
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibberellin; 18S rRNA; internal transcribed spacer region; ITS1; 5.8S rRNA; LTB-1027; species differentiation; GA_4; GA_3; GA_7; flowering; fruit cell elongation; apple; pear; grape; fruit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus M. microsporus, M. circinilloides f. circinelloides, Rhizopus oryzae, R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallesheria boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenkii. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi
                                                                                                                       misc_feature
                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gibberella fujikuroi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS16211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS16211 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               control; fungus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic DNA spanning 18S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \mathbf{\mu}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCCGGGCCTTGGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGCGGCGCCGCCACGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAG
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                   /*tag= b
/note= "ITS1 region"
1922. 2078
/*tag= c
/*tag= c rRNA ger
                                                                                                                                                                                               /note= "5.8S:
2079. .2243
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "18S rRNA gene"
1775. .1921
                                                                                                                       /note= "ITS2 region"
2244. .2293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
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                                               "28S rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.8S and 28S rRNA and ITS sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      racemosus, M. plumbeus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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RESULT 3
AAA61893
ID AAA6
XX
AC AAA6
XX
DT 15-S

standard; DNA;

502

2263

2203

241

301

2143 181 2090 2030

61

121

15-SEP-2003 AAA61893; AAA61893

(revised)

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Best Local S
Matches 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a genomic DNA sequence containing the 18S rRNA gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S rRNA sequences from a mutant strain of Gibberella fukikoroi (LTB-1027) of the invention. This region of DNA is highly variable and can be used for species and strain differentiation. The LTB-1027 mutant produces a mixture of gibberellins which is at least 70 % GA 4 and GA 7. Gibberellins GA 4 and GA 7 promote flowering and Fruit cell elongation, and are used by growers of apples, pears and grapes to produce larger fruits and earlier harvests. The mixture of GA 3, GA 4 and GA 7 achieved using the method of this invention should be particularly useful in the apple industry where GA 4 has been found more effective in russet control and in promoting fruit set. This method produces GA 4 and GA 7 in much higher titers than prior art methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A new method for producing a mixture of gibberellins from fujikuroi results in high titers of GA4 and GA7 useful to flowering and fruit growth in the fruit growing industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2293 BP; 596 A; 527 C; 592 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-662197/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-2001
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                                                             2204
                                                                                                                             2144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GALLAZZO J L.
LEE M D.
                                                                                                                                                                                                                                                        ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGC
                                                                                                                                                                                                                                                                            ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGC
                                                                                                                                                                                                                                                                                                                      AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
                                                                                                                                                                                                                                                                                                                                          AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
                     AATACCCGCTGAACTTAA
                                                                                 AGCGGCGCCGCCCGTAAAAACACCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG
                                                                                                                                               ATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAG
                                                                                                                                                                                                                AATACCCGCTGAACTTAA 2281
                                                               CGCGGCGCCGAAGCCGTTAAACCCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGG
                                                                                                                             ATCTAGTGGCGGTCTCGCTGCAGCTTCCATTGCGTAGTAAAAACCCTCGCAACTGGTA
                                                                                                                                                                                            CCCCGGGTTTGGTGTTGGGGATCGGCGAGCCCTTGCGGC-----AAGCCGGCCCCGAA
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0151770P
                                                                                                                                                                                                                                                                                                                                                                                                   76.6%;
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                              319
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 244.4;
Pred. No. 4.1
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other;
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14-NOV-2000

(first

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                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel steroid compounds derived from the African CC soil fungus Fusarium sp. MF6381 (ATCC 74469) which act as inhibitors of CC HIV integrase. The invention encompasses cultures of Fusarium sp. MF6381. CC The invention also relates to a composition comprising a compound of the invention in combination with an AIDS antiviral agent, an immunomodulator CC and an antiinfective agent. The compounds of the invention may be used in CC the inhibition of HIV integrase and in the prevention and treatment of CC HIV infection. A wide range of state of HIV infection may be treated: CC AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex); CC both symptomatic and asymptomatic HIV infection; and actual or potential CC exposure to HIV. The compounds may be used to isolate HIV integrase mutants which are potentially useful as screening tools for antiviral CC compounds. The compounds may also be used to establish or determine the site at which other antivirals bind to HIV integrase (e.g., by CC competitive inhibition). The present sequence represents the ribosomal CC MF6381, which may be used to characterise MF6381. (Updated on 15-SEP-2003 CC to standardise OS field)
                                                                                                                                                                                                                                                                   Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                   Sequence 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New steroid compounds are HIV integrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Singh SB, Zink DL,
Dombrowski AW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusarium sp; MF6381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     symptomatic infection; asymptomatic infection; potential HIV exposure; combination therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acquired immunodeficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribosomal DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusarium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osomal DNA; rDNA ITS region; internal compound; hume integrase inhibitor; steroid compound; hume AIDS; ARC;
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                                                                                                                                 ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGC
                  ATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAG 241
                                                                                    ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGC
                                                                                                                                                                                                ANAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
                                                                                                                                                                                                                       AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
ATCTAGTGGCGGTCTCGCTGCAGCCTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and AIDS.
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                 BP; 127 A; 144 C; 118
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                                                                                                                                                                                                                                                                                 75.8%;
88.2%;
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; Pred. No. 1.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
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                                                                                                                                                                                                                                                                                                                                 G; 113
                                                                                                                                                                                                                                                                                 1.6e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitors used for treating
                                                                                                                                                                                                                                                                                                                                 T; 0 U;
                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ranscribed spacer; ATCC 74469;
human immunodeficency virus;
hRC; AIDS-related complex;
                                                                                                                                                                                                                                                                  32;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel base sequence which is part of a fully defined riboscome ribonucleic acid (rRNA) gene of Cordyceps crassispora. The base sequences can be used for the classification of Cordyceps sinensis. The sequence represents a C. sinensis rRNA sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribosome RNA gene base sequence of Cordyceps sinensis for classification of seeds of Cordyceps sinensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. sinensis rRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Page 25; 33pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-639075/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HEAL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JAN-2001; 2001JP-00004805
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                                                                                                                                                                                                        379
493
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KANESHIRO N.
                                                                                                                                                                                                                                                                                                                                          ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCCTCAGGC
                                                                                                                                ATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCCTCGCAACTGGAG
                                                                                                                                                                                                                                  CCCCGGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCCAA
                                                                                                                                                                                                                                                                                                          ATTGCGCCCGCTGGTATTCCGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGC
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CGCGGCGCGCCATGCCGTAAAAC-CCCAACTTCTGAATGTTGACCTCGGATCAGGTAGG
                                                AGCGGCGCGCCACGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG
                                                                                                CCCCGGGTTTGGTGTTGGGGATCGGCTCTGCCTCACGGCGG----TGCCGCCCCGAA
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89.3%;
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Pred. No. 3.9
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hes 27;
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Best Local S
Matches 276
                                                                                                                                                                                                                                                                                                                                 This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods and primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present sequence represents an internal transcribed spacer RNA encoding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 38-39; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-2001; 2001US-00961755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondria; fungal pathogen; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYGN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Internal transcribed spacer RNA encoding sequence
                                                                                                                                                                                                                                                           Local Similarity
nes 276; Conserv
                                                   401
                                                                                                       348
                                                                                                                                                          288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYNGENTA PARTICIPATIONS
CGCGGCGCGCCAAGCCGTTAAACCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGG
              AGCGGCGGCCGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG
                                                                  ATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAG
                                                                                                                      CCCCGGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCCAA
                                                                                                                                                                       ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGC
                                                                                                                                                                                                                          AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
                                                                                                                                                                                                                                                                                                            534 BP; 135 A; 149 C; 130 G; 120 T; 0 U;
                                                ATCTAGTGGCGGTCTCGCTGCAGCTTCCATTGCGTAGTAAAAACCCCTCGCAACTGGTA
                                                                                                   CCCCGGGTTTGGTGTTGGGGATCGGCGAGCCCTTGCGGC-----AAGCCGGCCCCGAA
                                                                                                                                                      ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGC
                                                                                                                                                                                                        AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATACCCGCTGAACTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATACCCGCTGAACTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barnett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002WO-US030311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                      75.4%;
87.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534
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                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                       Score 240.4;
Pred. No. 4.9
                                                                                                                                                                                                                                                           Pred. No. 4.9
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G
                                                                                                                                                                                                                                                           1.9e-70;
nes 31;
                                                                                                                                                                                                                                                                                   DB
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                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                     534;
                                                                                                                                                                                                                                                           Gaps
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520
                        301
                                                460
                                                                          241
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63

TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGCC AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA AAATGCGATAAGTAATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTGAACGCACA Best Loc Matches Query Match

w

Local

Similarity

75.3**%**; 87.4**%**;

Conservative

0,

Pred. No. 4.6e 0; Mismatches Score

e 240.2; Db 2, 1. No. 4.6e-70; 1. No. 33;

Indels Length

7;

Gaps

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122

310;

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RESULT 6
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                                                                 which are species-specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans, F. Humigatus, A. niger, A. terreus, A. nidulans, M. circinilloides f. circinelloides, Rhizopus oryzae, R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallesharia boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenkii. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi. (Updated on 17-OCT-2003 to standardise os field)
      Sequence 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid probes for filamentous fungi - for detect
Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidi
Cunninghamella, Pseudoallescheria boydii, Penicillium and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus; M. racemosus; M. plumbeus; M. indicus; A. fumigatus; M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus; R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-034737/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Internal transcribed spacer 2 (ITS2) and adjacent regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2003
26-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence represents an internal transcribed spacer 2 (ITS2) adjacent regions. Probes can be derived from the present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      521
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      BP;
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   73 A; 86 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45pp; English.
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25-MAR-2003
06-JAN-1999
                   This sequence represents an internal transcribed spacer (ITS) sequence of the invention. The primer pairs, based on the ITS sequences, are used for the PCR amplification detection of wheat Microdochium and Fusarium funga pathogens, especially M. nivale, F. graminearum, F. culmorum, F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different strains of fungi show different symptoms during infection, which may or may not be due to infection. Barly identification of the strain causing the infection allows early, and more specific fungicidal treatment. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                           Wheat pathogen internal transcribed spacer sequences - used as for primers for the species-specific polymerase chain reaction of the pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beck
                                                                                                                                                                                                                                                         Claim 1; Col 29-30; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-593995/50
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athogen identification;
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                                                                                                                                                                                                                                 Ribosome
of seeds
                                                                  The invention relates to a novel base sequence which is part of a fully defined ribosome ribonucleic acid (rRMA) gene of Cordyceps crassispora. The base sequences can be used for the classification of Cordyceps sinensis. The sequence represents a C. crassispora rRNA sequence of the
                                                                                                                                                                                                                                                                                                                                              (HEAL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cordyceps crassispora.
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                                                                                                                                                                                                                                                                                                                                                                                                              12-JAN-2001; 2001JP-00004805
                                                                                                                                                                                 Page 12; 33pp; Japanese
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Pred. No. 6.8e-70;
2; Mismatches 27;
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17-FEB-1998
The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA gene from the filamentous fungi Trichoderma harzianum strain IMI 352940. A novel liquid formulation based on strains of T. harzianum and T. viride, has the following composition (w/v%): 0.1-6 sorbitol; 0.02-2
                                                                                                                                                                                                                                                      Liquid formulation of Trichoderma harzianum and Trichoderma viride strains - are used as biological control agents against diseases of plants and plant material and as biolixiviation agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITS1 ITS4 region; 5.8S rRNA; filamentous fungi; Trichoderma harzi liquid formulation; T. viride; gene recipient; increase activity; biological control agent; plant disease; biodeterioration; biolixiviation; leaching; ss.
                                                                                                                                                                                            Disclosure; Page 26;
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-280728/25
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    harzianum

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Pred. No. 6.8e-61;
0; Mismatches 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 268
                        12-JAN-2001;
                                                                                     23-JUL-2002
                                                                                                                   JP2002204696-A
                                                                                                                                                Cordyceps
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Pred. No. 7e-55;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  582
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                                                                                                                                                                                             Cordyceps
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                                                                                                                                                                                             crassispora;
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RESULT 11
AATG5101
ID AATG55
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XX AATG5
XX 17-PE
XX 17-FE
XX ITS1-
KW Liqui
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KW biole
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XX AG 15-M2
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Best Local :
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                                                                                                                                              ITS1-ITS4 region; 5.8S rRNA; filamentous fungi; Trichoderma harzianum; liquid formulation; T. viride; gene recipient; increase activity; biological control agent; plant disease; biodeterioration; biolixiviation; leaching; ss.
               07-NOV-1995;
                                       06-NOV-1996;
                                                                                            WO9716974-AJ
                                                                                                                       Hypocrea lixii; strain IMI 352941
                                                                                                                                                                                                                                            17-OCT-2003
17-FEB-1998
                                                                                                                                                                                                                                                                                    AAT65101;
                                                                                                                                                                                                                                                                                                           AAT65101 standard; DNA; 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel base sequence which is part of a fully defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispora. The base sequences can be used for the classification of Cordyceps sinensis. The sequence represents a C. sinensis rRNA sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Page
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                                                                   15-MAY-1997
                                                                                                                                                                                                                   harzianum
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KANESHIRO N.
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                                                                                                                                                                                                                                                                                                                                                                                             AATACCCGCTGAACTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \ensuremath{\mathsf{RNA}} gene base sequence of Cordyceps sinensis for classification of Cordyceps sinensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGGAGACGCTCACGCCCTAAAACGCCCCAACTTCTCAGAGTTGACCTCGGATCAGGTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCGGCGCCGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG
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                                                                                                                                                                                                             IMI 352941 5.8 S rRNA gene regions ITS1-ITS4.
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               95ES-00002266
                                        96WO-ES000206
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82.4%;
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                                                                                                                                                                                                                                                                                                             ВP
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Pred. No. 4.1e-53;
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RESULT 12
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AC AATO5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC A novel liquid formulation based on strains of T. harzianum and T. CC viride, has the following composition (m/v*): 0.1-6 sorbitol; 0.02-2 CC (X3PO3; 0.05-2 KNO3; 0.002-1 MgSO4.7H2O; 0.02-2 (NH4)H2PO4; 0.02-2 copper; CC 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron; 0.02-2 copper; CC 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron; 0.02-2 copper; CC 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron; 0.02-2 copper; CC 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron; 0.02-2 copper; CC 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron; 0.02-2 copper; CC 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-2 copper; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-2 iron; 0.02-2 copper; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-2 iron; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-2 iron; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-2 comper; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-2 copper; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-2 zinc; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-2 zinc; 0.02-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 272; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liquid formulation of Trichoderma harzianum and strains - are used as biological control agents plants and plant material and as biolixiviation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYSA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA gene from the filamentous fungi Trichoderma harzianum strain IMI 3529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 27; 37pp; Spanish.
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544
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                               CAGGTAGGAATACCCGCTGAACTTAA
                                                                                                CGGGAGCGCGGCGTCCACGTCCGTAAAACACCCCAACTTCTGAAATGTTGACCTCGGAT
                                                                                                                            CTGGAGAGCGGCGCGGCCACG-CCGTAAAACCACCCAACTTCTG-AATGTTGACCTCGAAT
                                                                                                                                                                                                GAAATACAGTGGCGGTCTCGCCGCAGCCTCTCCTGCGCAGTAGTTTGCACAACTCGACAC
                                                                                                                                                                                                                                  CAAATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGCTAACACCTC---GCAA
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CAGGTAGGAATACCCGCTGAACTTAA
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Pred. No. 2.1e-51;
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04-JUN-1996

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A novel method for the detection of plant pathogenic strains of fungi e.g. Septoria nodorum, S.tritici, Pseudocercosporella herpotrichoides, Mycosphaerella fijiensis, M.musicola or Fusarium spp. involves the PCR amplification of sequences found in the internal transcribed region (ITS) of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93 and AAT05357-72. These primers are derived from the ITS sequences of these fungi (AAT05394-T05404 and AAQ94398) and are strain specific. The amplification products of the reactions using these primers can be used with the capture primers AAT05378-93 in colourimetric assays. The primers and ITS DNAs can be used for the detection of specific fungal pathogen isolates and in monitoring disease development in plant populations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-NOV-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 54-55; 65pp;
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                                                                                                                                                                                                                                                                                                                                                                  271
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492
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                                                                                                                              accecceccadeccetapaadaccaacti
                                                                                                                                                                                                           ATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAG
                                                                                                                                                                                                                                                                                                                                                                                            ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
                                        AATACCCGCTGAA
                                                                                                                                                                              ATACATTGGCGGTCACGTCGRAGCTTCCATAGCGTAGTAATTTACATATCGTTACTGGTA
                                                                                                                                                                                                                                                                         CC---AGCTTGGTGTTGGGAGCTG-----
                                                                                                                                                                                                                                                                                                                    CCCCGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCCAA
                                                                                                                                                                                                                                                                                                                                                               ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beck JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intervening transcribed sequence - used for detection pathogens.  \label{eq:condition} % \begin{array}{ll} & & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ \end{array} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00233608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US004712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 132 C; 113 G; 122 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.6%;
81.5%;
504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 183.8; DB 2;
Pred. No. 4.3e-51;
1; Mismatches 38;
                                                                                        CCCAACTTCTGAATGTTGACCTCGGATCAGGTAGG
                                                                                                                                   CTGAATGTTGACCTCGAATCAGGTAGG
                                                                                                                                                                                                                                                                              ----CAGTCCTGCTGCACTCCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
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                                                                                          491
                                                                                                                                                                                                                                                                              372
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S 뮍 S

Best Local Similarity

57.6%; 81.5%;

Score Pred.

183. No.

4.3e-51;

Query Match

Sequence

504 B₽;

133 A; 132 C; 113

G; 122 T; 0 U; 4 Other;

Ś 밁 5

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ARBSULT 13
ANAC2591
ID ANAC2591
ANAC259
                                       This represents the consensus DNA sequence of the internal transcribed spacer (ITS) region that was PCR amplified from Fusarium culmorum isolates, R-5106, R-5126 and R-5146. The invention provides a DNA molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal pathogen, where the DNA molecule consists of an ITS sequence selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium moniliforme, Septoria avenae or Microdochicum nivale. A method for detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F. avenaceum and M. nivale isolates is also provided. The method comprises isolating DNA from a plant leaf infected with at least one of the above pathogens and amplifying parts of the ITS sequence of the pathogen(s) by PCR using specific primers from within these sequences. The pathogen(s) are detected by visualising the amplified part of the ITS sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV62591 standard; DNA; 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA isolated from fungal RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 3; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-541745/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beck
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15-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVS ) NOVARTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               avenae; Microdochicum nivale; Fusarium poae; Fusarium avenaceum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen; culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         culmorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid detection; ss.
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96US-00722187.
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/note= "5.8S
319. .472
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/note= "ITS
162. .318
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/note= "3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473. .504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= d
/note= "ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13. .161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "5' end of large subunit rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR amplified ITS region
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                                                                                                         Beck
This sequence represents an internal transcribed spacer (ITS) sequence of the invention. The primer pairs, based on the ITS sequences, are used for
                                                        Wheat pathogen internal transcribed spacer sequences - used as for primers for the species-specific polymerase chain reaction
                                                                                      WPI; 1998-593995/50
                                                                                                                                                04-AUG-1997;
                                                                                                                                                                  04-AUG-1997;
                                                                                                                                                                                     27-OCT-1998.
                                                                                                                                                                                                        US5827695-A.
                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                        Fusarium
                                                                                                                                                                                                                                                                                                                         Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen; fungal pathogen identification; infection identification; ss.
                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
06-JAN-1999
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                                                                                                                            (NOVS ) NOVARTIS
                                                                                                                                                                                                                                                                                                                                                        culmorum
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                                                                                                                                                                                                                                                                                                        culmorum.
                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATACCCGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATACCCGCTGAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCGTCGCGGCYACGCCGTTAAAC-CCCAACTTCTGAATGTTGACCTCGGATCAGGTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCGGCGGCGCCACGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATACATTGGCGGTCACGTCGRAGCTTCCATAGCGTAGTAATTTACATATCGTTACTGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC---AGCTTGGTGTTGGGAGCTG------CAGTCCTGCTGCACTCCCAA
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                                                                                                                                                                                                                                                                                                                                                      internal transcribed spacer
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(first en
                                                                                                                                                97US-00905314.
                                                                                                                                                                  97US-00905314
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/note= "ITS1"
319. 472
                              21-22;
                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                            FINANCE CORP
                                                                                                                                                                                                                            note= "ITS2"
                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                            . 161
                            20pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
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                             English
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detection
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RESULT 15
ACC49999
XX ACC49
XX ACC49
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XX Inter
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Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.

밁 Ş g δ 유 밁 Ş 8X22222X8 В Ś 밁 Ş Query Match 57.4%; Score 183.2; DB 7; Length 522; Best Local Similarity 83.4%; Pred. No. 7e-51; Matches 262; Conservative 0; Mismatches 33; Indels 19; This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods and primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present sequence represents an internal transcribed spacer RNA encoding sequence Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other; Claim 5; Page 38; 44pp; English. 509 302 391 ATTGATTGGCGGTCACGTCG-AGCTTCCATAGCGTAGTAGTAAAACCCTCGTTACTGGTA 182 348 122 CCCCGGGCCTGGCGTTGGGGATTCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCAA 181 288 228 AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC 287 62 2 AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC 61 AATACCCGCTGAAC 522 AATACCCGCTGAAC 315 ATACAGTGGCGGTCCCGCCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAG 241 CC---AGCTTGGTGTTGGGACTC------GCGAGTCAAATCGCGTTCCCCCAA ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGC ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGC Gaps 449 390 347 121 4

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Sequence 7, Application US/09423233

Patent No. 6372430

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Uncleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: 0.0043/1WP
CURRENT APPLICATION NUMBER: US/09/423,233

CURRENT FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 61

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7

LENGTH: 310
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: ORGANISM: Fusarium moniliforme
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                                                                Query Match
Best Local Similarity
Matches 277; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 2293
TYPE: DNA
ORGANISM: Gibberella fujikuroi
S-09-645-073-1
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/645,073
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,770
PRIOR FILING DATE: 199-08-31
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lee, May
APPLICANT: Galazzo, Jorge
TITLE OF INVENTION:

**TOP-01UP
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AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
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ilarity 87.4%;
Conservative
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88.1%;
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                                                                °.
                                                              Score 240.2; DB 4
Pred. No. 1.1e-68;
0; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 244.4; DB 3;
Pred. No. 1.1e-69;
0; Mismatches 31;
                                                                                                   DB 4;
                                                                33;
                                                                                                   Length 310;
                                                                Indels
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEPHONE: (919) 541-8689
INFORMATION FOR SEO ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-905-314A-24
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                                                                                                                                                                  MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECT
TITLE OF INVENTION: USING
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NAME/KEY:
LOCATION:
                                                                                NAME/KEY:
LOCATION:
                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                  STRAIN:
                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: li
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                 STRAIN: Fusarium avenaceum INDIVIDUAL ISOLATE: 64452
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RESULT 5
US-08-652-127C-6
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Best Local S
Matches 282
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08652127C Patent No. 5792611
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Richard
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GEOTGE A. Seaby
REGISTRATION NUMBER: 24,034
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
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FEATURE:
NAME/KEY: misc_fea
LOCATION: 182.338
                                                                                                                                                                                                                                    STREET: 880 We CITY: Ottawa
                                                                                                                                                                                                         ZIP:
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OTHER INFORMATION: /not
                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                    ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby & MacLean
STREET: 880 Wellington Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: 505...561
OTHER INFORMATION: /note= "5'
OTHER INFORMATION: rRNA gene"
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                                                                                                                                                                                                           K1R 6K7
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                                                                                                                                                                                                                                                                                                                                           Richard C. Hamelin
VENTION: DETECTION OF PLANT
VENTION: PATHOGEN FUNGI
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88.7%;
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US-08-652-127C-7
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Patent No. 5792611
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 272; Conserv
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEPAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
NAME: GEORGE A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1899
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
                                                                                                              SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: May 23, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                                                                                                                                   STREET: 880 V
                                                                                                                                                                                                                                                                                                   COUNTRY:
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STRANDEDNESS: doub.
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                                                                                                                                                                                                                                                                                                                                      880 Wellington Street, Suite 708
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Seaby & MacLean
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85.5%;
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,127C

FILING DATE: May 23, 1996

CLASSIFICATION: 435

CLASSIFICATION 1005

ATTORNEY/AGENT INFORMATION:

NAME: GEOTGE A. Seaby

REGISTRATION NUMBER: 24,034

REFERENCE/DOCKET NUMBER: 1898

TELECOMMUNICATION INFORMATION:

TELEPAX: (613) 232-5815

TELEPAX: (613) 232-5815

TELEPAX: (613) 232-5815

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
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US-08-652-127C-8
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 531
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ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby & MacLean
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TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                       880 Wellington Street, Suite 708
                                                                                                                                                                                                                                                                                                                                                                                                       Canada
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85.2%;
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RESULT 8
US-08-652-127C-5
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Patent No. 5792611
GENERAL INFORMATION:
                                                                 TELEFAX: (613) 232-5831 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 272; Conserv
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                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/6
FILING DATE: May 23, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                            ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                STRANDEDNESS:
                              TYPE: nucleic acid
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                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: George A. Seaby ADDRESSEE: Seaby & MacLean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377
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                                                                                                                                                                                                                                                                                                                                                                                                                                  880 Wellington Street, Suite 708
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IBM PC Compatible
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linear
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Pred. No. 1.3e-58;
0; Mismatches 34
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RESULT 9
US-08-887-480-82
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Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 268; Conservative
                                                                                                                       TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            FILING DATE: 15-OCT-1996
ATTORNEY AGENT INFORMATION:
NAME: Medge, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
 ORGANISM:
                                               LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Tarrytown
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Fusarium culmorum
                                DNA (genomic)
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83.2%;
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RESULT 10
US-08-905-314A-19
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                                                                                                                                                                       Sequence 19, Application US/08905314A
Patent No. 5827695
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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INDIVIDUAL
FEATURE:
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827695artis Corporation Patent Department STREET: 3054 Cornwallis Road
                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: FEATURE:
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                                                                       CITY: Research Triangle Park STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: 473.504
OTHER INFORMATION: /note= "5'
OTHER INFORMATION: xRNA gene"
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                                                       COUNTRY:
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                                                         USA
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81.5%;
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rRNA gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 183.8; DB 1
Pred. No. 2.9e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "ITS
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US-08-905-314A-19
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Matches
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEPAX: (919) 541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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OTHER INFORMATION: /note OTHER INFORMATION: rRNA
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
mes 255; Conserv
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OTHER INFORMATION: /note=
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 319..472
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LOCATION: 162..318
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CLASSIFICATION: 435
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   433
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                     AGCGGCGGCGGCACGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG
                                                                   ATACATTGGCGGTCACGTCGRAGCTTCCATAGCGTAGTAATTTACATATCGTTACTGGTA 432
                                                                                                                                           CC---AGCTTGGTGTTGGGAGCTG-------CAGTCCTGCTGCACTCCCCAA
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ATCGTCGCGGCYACGCCGTTAAAC-CCCAACTTCTGAATGTTGACCTCGGATCAGGTAGG
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81.5%;
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rRNA gene"
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rRNA gene"
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Pred. No. 2.9e-50;
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US-08-722-187-82
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TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
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APPLICANT: Ligon, James
APPLICANT: Beck, James
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NAME/KEY: misc_feature

1.504

1.7001

1.504
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REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
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FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Detection of Fungal Pathogens Using the TITLE OF INVENTION: Polymerase Chain Reaction NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                  LOCATION: 1..504
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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COUNTRY:
                                                                                                                                                                                                                   Local Similarity
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CLASSIFICATION: 435
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CITY: Hawthorne
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                                                                                                                                211 AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
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                               CCCCGGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCAA 181
 CC---AGCTTGGTGTTGGGAGCTG--
                                                                                               ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGC 121
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81.5%;
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internal transcribed spacer region of Fusarium culmorum
(fculm.con)"
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Pred. No. 2.9e-50;
1; Mismatches 38
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-----CAGTCCTGCTGCACTCCCCAA
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NAME/KEY: misc feat:
LOCATION: 1.504
COTHER INFORMATION:
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PCT-US95-04712-82
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Best Local Similarity 81.5
Conservative
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 08/233
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Beck, James J
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62 ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGC 121
                                                       2 AAAATGCGATAAGTAATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTGAACGCAC 61
                                  AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC 270
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81.5%;
                                                                                                                                                                                                  /note= "DNA sequence for the
internal transcribed spacer region of Fusarium culmorum
(fculm.con)"
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                                                                                                        Score 183.8; DB 5; Length Pred. No. 2.9e-50; 1; Mismatches 38; Indels
                                                                                                          19;
                                                                                                        Gaps
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RESULT 13
US-08-887-480-84
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                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                    TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
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APPLICANT: Beck,
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MEDLUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT Application DATA:
APPLICATION NUMBER: US/08/887,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Beck, Ja
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                              INDIVIDUAL ISOLATE: IMMEDIATE SOURCE:
                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 545 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
 NAME/KEY: misc feature LOCATION: 1..30
OTHER INFORMATION: /note OTHER INFORMATION: rRNA
                                                                                                                                                                                                          TOPOLOGY:
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CLASSIFICATION:
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                                                                                                                                                       ORGANISM:
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o. 5814453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of Fungal Pathogens Using the Polymerase Chain Reaction
/note= "3' end of small subunit rRNA gene"
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                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827695artis Corporation Patent Department
STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                          APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
APPLICATION NUMBER: US/08/905,314A FILING DATE: CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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OTHER INFORMATION: /notFEATURE:
                                                                                                                                                                                            STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                            COUNTRY: USA
ZIP: 20779-2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 489..545
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
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336..488
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82.4%;
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RESULT 15

US-08-887-480-96

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FEATURE: misc feat;
NAME/KEY: misc feat;
LOCATION: 489...545;
OTHER INFORMATION: //
OTHER INFORMATION: //
US-08-905-314A-21
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TELEPAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
LENGTH: 545 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                     Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OKGANISM: FUBATIUM MODILIFORME INDIVIDUAL ISOLATE: 4551
IMMEDIATE SOURCE: CLONE: pCRFMON1
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241 REFERENCE/DOCKET NUMBER: CGC TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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COTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION: /note
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OTHER INFORMATION:
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LOCATION: 336..488
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                            AATACCCGCTGAACTTAA 319
                                                                          AGCGGCGCGGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG 301
                                                                                                                                 ATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAG
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                                                                                                                                                                                                                                   ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGC
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AATACCCGCTGAACTTAA
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rRNA gene"
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Pred. No. 3.8e-49;
0; Mismatches 36
525
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US-08-887-480-96
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ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38, 241
REFERENCE/DOCKET NUMBER: CGC 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5814453
PATENT NO. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
TITLE OF INVENTION: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 96, Application US/08887480 Patent No. 5814453
                                                                                                                                                                                                                                                                                                                                                                             CLONE: PCRFPULL-
CLONE: PCRFPULL-
FEATURE: misc feature
NAME/KEY: misc feature
1.30
1.30
/note
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IMMEDIATE SOURCE:
CLONE: pCRFpoaer4^~~'.
                                                                                                                                                                                                                                        OTHER INFORMATION:
FEATURE:
NAME/KEY: misc_fea
                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/887,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                         NAME/KEY:
LOCATION:
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                                                                   NAME/KEY: misc feature LOCATION: 490..546
OTHER INFORMATION: /note OTHER INFORMATION: rRNA
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                                                                                                                                                       OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 31..180
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338..489
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181..337
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56.4%;
82.4%;
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rRNA gene"
                                                                /note= "5' end of large subunit rRNA gene"
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Score 180; DB 1;
Pred. No. 5.2e-49;
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Search completed: October 1, 2004, 08:05:39
Job time: 110.125 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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seq length: 2000000000
Published Applications NA:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11 11 11 11 11 11 11 11 11 11	Result No.
319 240.4 240.2 183.2 176.3 131.8 131.8 131.8 1123.6 123.6 1129.8 119.8 119.8	Score
100.0 75.4 75.3 57.4 55.3 41.3 41.3 39.6 38.6 37.6 37.6	Query Match
319 522 522 522 522 521 521 365 365 650 650	Length
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US-10-046-955-6 US-09-961-755A-7 US-10-046-955-7 US-09-961-755A-8 US-09-961-755A-6 US-09-961-755A-6 US-10-121-740-2 US-10-623-432-2 US-10-046-955-3 US-10-046-955-2 US-10-046-955-2 US-10-046-955-2 US-10-121-740-4 US-10-623-432-4 US-09-766-173C-4	ID
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US-10-424-599-82575	115-10-083-357-360	US-10-43/-963-59964	US-10-046-955-12	US-10-046-955-8	US-10-046-955-9	US-10-046-955-10	US-10-083-357-372	US-10-358-929A-3	US-10-297-621-2	US-10-358-929A-5	US-10-358-929A-4	US-10-083-357-71	US-10-083-357-72	US-10-046-955-4	US-10-254-657-1	US-09-961-663-18	US-09-961-663-17	US-09-961-663-19	US-09-961-663-16	US-09-961-663-15	US-09-961-663-14	US-10-046-955-29	US-10-356-320-1	US-10-046-955-28	US-10-046-955-25	US-10-046-955-26	US-10-046-955-27	US-09-766-173C-5	
Sequence 82575, A		Sequence 59964, A	12		9		37	w	2	'n	4.	71	72	Sequence 4, Appli	e 1,		Sequence 17, Appl	19,	16,	15	Sequence 14, Appl	Ŋ	_	28,	25,		Sequence 27, Appl	Sequence 5, Appli	

ALIGNMENTS

```
APPLICANT: Choi, Jong Soo
TITIE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITIE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 1909-05-01
PRIOR FILING DATE: 1999-05-01
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-10-046-955-6
                                                                                                  US-10-046-955-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 6, Application US/10046955; Publication No. US20030129600A1; GENERAL INFORMATION:
                                                                                                                                                                   SEQ ID NO 6
LENGTH: 3
    Matches
                        Best Local
                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dist APPLICANT: Control and Prevention APPLICANT: Morrison, Christine J. APPLICANT: Morrison, Christine J. APPLICANT: Reiss, Errol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                               TYPE: DNA
ORGANISM: Fusarium solani
    319;
                                                                                                                                                                     319
                           Similarity
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100.0%; Score 319; DB 15; llarity 100.0%; Pred. No. 1e-104; Conservative 0; Mismatches 0;
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                                               Length 319;
    Indels
    <u>,</u>
  Gaps
    0
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RESULT 2
US-09-961-755A-7
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Publication No. US2030113722A1
GENERAL INFORMATION:
APPLICANT: Beck, Jim
APPLICANT: Beck, Jim
APPLICANT: Beck, Jim
TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 60055
CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
SOFTWARDE: Detection 3 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 534
TYPE: DNA
ORGANISM: Fusarium proliferatum
S-09-961-755A-7
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Best Local Similarity
Matches 276; Conserv
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                          AATACCCGCTGAAC 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 240.4; DB 10;
Pred. No. 3.6e-76;
0; Mismatches 31;
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RESULT 3

SOFTWARE:

PatentIn version 3.0

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CURRENT APPLICATION NUMBER: US/10/046,955;
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233;
PRIOR FILING DATE: 2000-06-27;
PRIOR PILING DATE: 1900-06-27
PRIOR FILING DATE: 1998-05-01
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                       RESULT 4
US-09-961-755A-5
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; ORGANISM: Fusarium moniliforme
US-10-046-955-7
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                                                                                                                                                                    Sequence 5, Application US/09961755A Publication No. US20030113722A1 GENERAL INFORMATION:
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Best Local S
Matches 277
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APPLICANT: Beck, Jim
APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Fusarium Species
TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 60055
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Aidorevich, Liliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dist APPLICANT: Control and Prevention APPLICANT: Morrison, Christine J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                          ATACCCGCTGAACTTAA
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Pred. No. 3.3e-76;
0; Mismatches 33;
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US-09-961-755A-8
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                                                                                                                                                                                                                                                                                     APPLICANT: Beck, Jim
APPLICANT: Beck, Jim
APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 60055
CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 522
TYPE: DNA
ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09961755A Publication No. US20030113722A1 GENERAL INFORMATION:
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Best Local Similarity 83.4%;
Matches 262; Conservative
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262;
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Similarity 83.4%;
62; Conservative
   ATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAG
                                                                                                           ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGC
                                                                                                                               ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGC 121
                                                  CC---AGCTTGGTGTTGGGACTC
                                                                      CCCCGGGCCTGGCGTTGGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCCAA 181
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Pred. No. 1.8e-55;
0; Mismatches 33
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Pred. No. 1.8e-55;
0; Mismatches 33
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RESULT 7

US-10-121-740-2

Sequence 2, Application US/10121740

Publication No. US20030186425A1

GENERAL INFORMATION:
APPLICANT: Strobel, Gary
APPLICANT: Strobel, Gary
ITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
ITLE OF INVENTION: USE
ITILE OF INVENTION: USE
CURRENT APPLICATION UNMBER: US/10/121,740
CURRENT FILLING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/283,902
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; TYPE: DNA
; ORGANISM: Gibberella zeae
US-09-961-755A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-961-755A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Beck, Jim
APPLICANT: Barnett, Jason
APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using
TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 60055
CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09961755A Publication No. US20030113722A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 258; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             288 ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AAAATGCGATAAGTAATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTGAACGCAC 61
                                 AATACCCGCTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGC 121
                                                                                                                                     AGCGGCGCGCCACCGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGG 301
                                                                                                                                                                                                                ATACATTGGCGGTCACGTCG-AGCTTCCATAGCGTAGTAATTTACACATCGTTACTGGTA 448
                                                                                                                                                                                                                                              ATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAG 241
                                                                                                                                                                                                                                                                                                                                                                   CCCCGGGCCTGGCGTTGGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCCAA 181
AATACCCGCTGAAC
                                                                                                         ATCGTCGCGGCCACGCCGTTAAAC-CCCAACTTCTGAATGTTGACCTCGGATCAGGTAGG
                                                                                                                                                                                                                                                                                                                       CC---AGCTTGGTGTTGGGAGCTG-----CAGTCCTGCTGCACTCCCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.3%;
ilarity 82.2%;
Conservative
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521
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Pred. No. 5.2e-53;
0; Mismatches 36; 1
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OF.

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DЬ
                                                                                                                                            ; SEQ ID NO 2
; LENGTH: 652
; TYPE: DNA
; TYPE: DNA
; ORGANISM: Muscodor a
US-10-623-432-2
                                                                                                                                                                                                                        APPLICANT: Strobel, Gary
APPLICANT: Manker, Denise
TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
TITLE OF INVENTION: USE
FILE REFERENCE: AQ 2019-40
CURRENT APPLICATION NUMBER: US/10/623,432
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: US/10/121,740
PRIOR PILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/383,902
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: 60/363,072
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASLSEQ for Windows Version 4.0
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; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 2
; LENGTH: 652
; TYPE: DNA
ORGANISM: Muscodor albus
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US-10-623-432-2
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                                                                           Matches
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10623432 Publication No. US20040141955A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 41.3%;
Best Local Similarity 72.6%;
Matches 230; Conservative
                                                                                        Local Similarity
                                                                          230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 TACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGCTAACACCTCGCAACTGGAGA
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                      3 AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTTGAACGCACA 62
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AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATACCCCCTGAACTTAA 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTTCCGGCCCCTGCCCTAAAAACCCCCCTATATC-AAAGGTTGACCTCGGATCAGGTAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGCGCCCGCCAGTATTCTGGCCGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGCC 122
                                                                          Conservative
                                                                                                                                                                 albus
                                                                                        41.3%;
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                                                                      Score 131.8; DB 17;
Pred. No. 7.9e-37;
0; Mismatches 72;
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Pred. No. 7.9e-37;
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                                                                                                     Length
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                                                                  Gaps
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CURRENT APPLICATION NUMBER: US/00/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
LENGTH: 365
TYPE: DNA
ORGANISM: Aspergillus niger
US-10-046-955-3
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US-10-046-955-3
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Publication No. US20030129600A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the APPLICANT:
Secretary of the Department of Health and Human Services, Centers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205;
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                                                                                                                                                                                                                                                                                                                                                                                                         52 AAATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
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Similarity 64.7%;
                                                            TACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAGA 242
                                                                                                                                                                                                                                                                 TTGCGCCCCCGGTATTCCGGGGGGGATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCA 171
GGCGGCACCGCGTCCGATCCTCGAGCGTATGGGGCCTTTGTCACCTGCTCTGTAGGCCCGG
                                                                                                                                                                                             сссерестрестрефентов по температурного по темпер
                                                                                                                                                                                                                                                                                                                                  TIGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGCC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATACCCGCTGAACTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ccceeeccreecerreeearreeeceaeaaaecccccreeeeceacaaceaccercccccaaa 182
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Reiss, Errol
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RESULT 11
US-10-046-955-2
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US-10-046-955-5
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PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Aidorevich, Liliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
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TYPE: DNA
ORGANISM: Aspergillus nidulans
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US-10-121-740-4
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                             APPLICANT: Strobel, Gary
APPLICANT: Manker, Denise
TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS
TITLE OF INVENTION: USE
FILE REFERENCE: AQ 2019.40
CURRENT APPLICATION NUMBER: US/10/121,740
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/883,902
PRIOR FILING DATE: 2002-03-11
                 PRIOR APPLICATION NUMBER: 60/363,072 PRIOR FILING DATE: 2001-04-16
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 SEQ ID NOS: 4
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; LENGTH: 364
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-046-955-2
Sequence 4, Application US/10121740 Publication No. US20030186425A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
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PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR APPLICATION NUMBER: US 60/045,400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species TITLE OF INVENTION: Other Filamentous Fungi
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APPLICANT:
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CURRENT FILING DATE: 2002-06-04
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                                                                                                                                                                                                                                                                284 CCCGGCCGGCCAGCCGACACCCAACTTTATTTTTCTAAGGTTGACCTCGGATCAGGTA
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                                                                                                                                                                                                                                                                                                         GCGGCGCGCGCACGCCGTAAAACACCC---AACTTCTGAATGTTGACCTCGAATCAGGTA 299
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Pred. No. 4.2e-33;
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RESULT 13

US-10-623-432-4

i Sequence 4, Application US/10623432

i Publication No. US20040141955A1

i GENERAL INFORMATION:
   APPLICANT: Strobel, Gary
   APPLICANT: Strobel, Gary
   APPLICANT: Strobel, Gary
   APPLICANT: STROBER: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
   TITLE OF INVENTION: USE
   FILE REPERENCE: AQ 2019.40

CURRENT APPLICATION NUMBER: US/10/623,432

CURRENT APPLICATION NUMBER: US/10/121,740

PRIOR APPLICATION NUMBER: US/10/121,740

PRIOR APPLICATION NUMBER: 60/283,902

PRIOR FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: 60/383,902

PRIOR FILING DATE: 2001-04-16

i NUMBER: OF SEQ ID NOS: 4

SOFTWARE: FRISTRO FOR WINGER: 40/363,072
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                                                                                                                                                                                        ; LENGTH: 650
; TYPE: DNA
; ORGANISM: Muscodor roseus
US-10-623-432-4
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; ORGANISM: Muscodor
US-10-121-740-4
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                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version SEQ ID NO 4
LENGTH: 650
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Best Local
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Matches 229;
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                     TIGCGCCCGCCAGTATICTGGCGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGCC 122
TTGCGCCCATTAGCATTCTAGTGGGCATGCCTGTTCGAGCGTCATT-TACCACTTAAGCC
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nilarity 72.2%;
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                                                                                                                        Score 119.8; DB 17;
Pred. No. 1.7e-32;
0; Mismatches 72;
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Pred. No. 1.7e-32;
0; Mismatches 72;
                                                                                                                                                     DB 17;
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GENERAL INFORMATION:

APPLICANT: Carroll, George C.

TITLE OF INVENTION: Materials and Methods For Detection of TITLE OF INVENTION: Pathogenic Guignardia Citricarpa FILE REFERENCE: Oregon 99-09

CURRENT APPLICATION NUMBER: US/09/766,173C

CURRENT FILING DATE: 2001-01-22

PRIOR APPLICATION NUMBER: PCT/US01/01735

PRIOR FILING DATE: 2001-01-19

PRIOR FILING DATE: 2001-01-19

PRIOR FILING DATE: 2001-01-19

NUMBER OF ESQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Guignardia
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al Similarity 62.5%;
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ATACCCGCTGAACTTAA 628
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Pred. No. 1.8e-30;
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RESULT 15 US-10-046-955-24

Sequence

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Application US/10046955

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CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: DS 60/045,400
PRIOR FILING DATE: 1997-05-02
PRIOR FILING DATE: 1998-05-01
PRIOR FILING DATE: 1998-05-01
PRIOR FILING DATE: 1998-05-01
PRIOR FILING DATE: 1998-05-01
PRIOR FILING DATE: 1998-05-02
PRIOR FILING DATE: 1998-05-03
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Search completed: October Job time : 1304.11 secs
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APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention APPLICANT: Morrison, Christine J. APPLICANT: Reiss, Errol

APPLICANT: Aidorevich, Liliana APPLICANT: Choi, Jong Soo

TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and TITLE OF INVENTION: Other Filamentous Fungi

FILE REFERENCE: 6395-62064

CURRENT FILING DATE: 2002-06-04

CURRENT FILING DATE: 2002-06-04

CURRENT FILING DATE: 2002-06-04

CURRENT FILING DATE: 2002-06-04
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Best Local Similarity
Matches 244; Conserva
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                                                                                                                                                                                301
                                                                                                                                                                                                               278 AA----TGTTGACCTCGAATCAGGTAGGAATACCCGCTGAACTTAA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 GCC----GTCCCCCAAATACAGTGGCGGTCCCGCCGCCGCGGTGCTTCCAT-TGCGTAGTAGCTA 224
                                                                                                                                                                                                                                                                                                                                              241 TETTTTGCAAGETEĞEATTGĞĞTECEGĞEGĞAĞĞEETGCEGTEAAACEAEETAACAAETE
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ALIGNMENTS

JOURNAL COMMENT ACCESSION VERSION KEYWORDS RESULT 1 CF870552 LOCUS SOURCE ORGANISM REFERENCE DEFINITION TITLE AUTHORS Analysis of the protein processing and se Trichoderma reesei EST dataset Unpublished (2003)
Contact: Ralph A. Dean Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph dean@ncsu.edu
Seq primer: LT-F1 primer. Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 739)
Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,
Motchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and 739 bp mRNA linear EST 31-OCT-2003 tric024xb14.bl T.reesei mycelial culture, Version 6 October 2003 Hypocrea jecorina cDNA clone tric024xb14, mRNA sequence.
CF870552 EST Dean, R.A. CF870552.1 GI:38125234 secretion pathways in

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JOURNAL COMMENT
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                                                                          Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 270
Tel: 919-513-0020
Fax: 919-513-0024
                                                                                                                                                                                                                                            Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 755)
Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,
Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and
                    Email: ralph_dean@ncsu.edu
Seq_primer: LT-F1 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   T55 bp mRNA trico24xj04.bl T.reesei mycelial culture, Hypotrea jecorina cDNA clone tric024xj04, CF870665
                                                                                                                                                                Contact: Ralph A. Dean
                                                                                                                                                                                  Trichoderma reesei
Unpublished (2003)
                                                                                                                                                                                                 Analysis of the protein processing and Trichoderma reesei EST dataset
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/clone_lib="T.reesei mycelial culture, Version 6 October
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/mol_type="mRNA"
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/clone="tric024xb14"
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source
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             Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto,
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-Fl primer.
Location/Qualifiers
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                                                                                                                                                                                    Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S., Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J., Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C., Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M. Transcriptional regulation of biomass-degrading enzymes in the filamentous fungus Trichoderma reesei J. Biol. Chem. 278 (34), 31988-31997 (2003)
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tric024xb14 T.reesei mycelial culture, Version 3 april Hypocrea
jecorina cDNA clone tric024xb14, mRNA sequence.
CB900742
                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (bases 1 to 796)
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Hypocrea jecorina
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/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version
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/strain="QM6a"
/db_xref="taxon:51453"
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Pred. No. 8.6e-39;
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                                                                                        Genencor Intl.
925 Page Mill Road, I
Tel: (650) 846-7635
Fax: (650) 621-7817
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                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
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Hypocrea jecorina
                                                                                                                                                               Contact: Pamela
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                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 808)
                                                   il: Pforeman@genencor.com
primer: LT-F1 primer.
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/db_xref="taxon:51453"
/clone="tric024xb14"
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/mol_type="mRNA"
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                                                                                                                                                                 K. Foreman
                                                                                                                             Palo Alto,
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Pred. No. 8.8e-39;
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Best Local Similarity
Matches 269; Conserv
                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                     Trichoderma reesei EST dataset
Unpublished (2003)
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, U
Tel: 919-513-0020
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Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (bases 1 to 735)
Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,
Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and
                                                                     Fax: 919-513-0024
Email: ralph dean@ncsu.edu
Seq primer: LT-F1 primer
Location/Qualifiers
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Trichoderma reesei EST dataset
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGGCGTCATTACAACCCTCAGGCC 122
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/clone="tric024x;04"
/dev_stage="mycelia"
/clone lib="T.reesei mycelial culture, Version 3 april"
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
              organism="Hypocrea
/mol_type="mRNA"
/strain="QM6a"
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/strain="QM6a"
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83.8%;
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                                    jecorina"
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Version 6 October 2003
mRNA sequence.
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22803314
12788920
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925 Page Mill Road, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 840)
Foreman, P. K., Brown, D. E., Dankmeyer, L., Dean, R., Diener, S., Dunn-Coleman, N. S., Goedegebuur, F., Hoofek, F.D., Bngland, G.J., Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C., Colivares, H.A., Teunissen, P.J., Yao, J. and Ward, M. Transcriptional regulation of blomass-degrading enzymes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     840 bp mRNA linear EST 02-JUL-.
tric081xc18 T.reesei mycelial culture, Version 3 april Hypocrea
jecorina cDNA clone tric081xc18, mRNA sequence.
                                                                                                                                                                            Seq
                                                                                                                                                                                        Email: Pforeman@genencor.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Hypocreaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       w
                                                                                                                                                                                                                                                                                                                                 filamentous fungus
J. Biol. Chem. 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB907036.1 GI:30121694
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                                                                                                                                                      primer: LT-F1 primer.
    Location/Qualifiers
                                                                                                                                                                                                            (650) 846-7635
(650) 621-7817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                              Pamela K.
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial c
/note="Vector: pREP3Y; Site_1:
                                                                                                         /mol
                                                    /strain="QM6a"
/db_xref="taxon:51453"
/clone="tric081xc18"
                                                                                                      organism="Hypocrea jecorina"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
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/dev_stage="mycelia"
/clone_lib="T.reesei
2003"
                                                                                                                                           .840
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79.9%;
                                                                                                                                                                                                                                                                              Foreman
                                                                                                                                                                                                                                                                                                                             Trichoderma reesei (34), 31988-31997 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 139.4; 1
Pred. No. 5.5e
0; Mismatches
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culture, Version 3 apr
: Not I/Sal I; Mycelial
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ESTs from mycelia of Colletotrichum trifolii race 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAD1/TV Mora
www.medicago.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford
Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Other_ESTs: EST631847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Deborah A.
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Colletotrichum trifolii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTCCGAGCGTCATTTCAACCCTCGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGCGCCCGCCAGTATICTGGGCGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCGGCGCCGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACAGNGGCGGTCTCGCCGCACCCTTTTCTGCGCAGCTACTTGCACACTCTCACCCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC---TCCGGGGGTCGGTTTTGGGGATCGGCCCCT----CACCGGGCCGCCCCCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCGGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCAAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 704)
                                                                                                                                                                                                                                                                                                                                                                                                        primer: (gtA AtA CgA CtC
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
/tissue_type="mycelia"
/dev. stage="Young, actively growing mycelia (3 days af inoculation) grown in liquid culture (cutin minimal_mecontaining 2%glucose)."
/lab host="DRST"
/clome_lib="DSCT"
/clome_lib="DSCT"
/clome_lib="DSCT"
/stage="DSCT"
/clome_lib="DSCT"
/clo
                                                                                                                                                                                                                                /db_xref="taxon:5466"
/clone="pDSCT4-17"
                                                                                                                                                                                                                                                                                           mol_type="mRNA"
strain="race 1"
                                                                                                                                                                                                                                                                                                                                                   organism="Colletotrichum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.7%;
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Pred. No. 5.8e-27
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m trifolii cDNA clone
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pDSCT4-17, mRNA
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                                                                                                                                             minimal_medium
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                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Other EST8: EST632563
CONTACT: Deborah A. Samac
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
University of Minnesota
195 Borlaug Hall, 1991 Upper Buford Circle,
                                                                                                                                                                                                                                                                                                                                                                                                                                Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T. Cheung,F. and Fraser,C.M.
BSTs from mycelia of Colletotrichum trifolii race 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.
                                                                                                                                                                                                                    Email: debbys@puccini.crl.umn.
TIGR sequence name: MTSAI22TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ752001 725 k
EST632564 DSCT Colletotrichum
                                                                                                                                                                                              www.medicago.org
                                                                                                                                                                                                                                                              Tel: 612 625 1243
Fax: 651 649 5058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTGCGGGCACAACGCCGTCCCCCAAATACAGTGGCGGTCCCGC-CGCAGCTTCCATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 725)
                                                                                                                                                      primer: (gtA AtA CgA CtC
    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enriched RNA The cDNA was ligated into Lambda gt11 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which
/db_xref="taxon:5466"
/clone="pDSCT9-22"
/tissue_type="mycelia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    were plated onto medium with X-gal for selection of recombinants."
                                                                      mol_type="mRNA"
strain="race 1"
                                                                                                          organism="Colletotrichum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:21907406
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77.6%;
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Pred. No. 5.5
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m trifolii cDNA clone pDSCT9-22, mRNA
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More information
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                                                                                                                                                                                                                                                                                                        Paul,
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REFERENCE AUTHORS

TITLE

FEATURES

FEATURES

COMMENT

TITLE AUTHORS

JOURNAL

REFERENCE

ACCESSION VERSION KEYWORDS

RESULT 9 BQ751015 LOCUS

KEYWORDS VERSION ACCESSION 밁 Ś 밁 S 밁 8 밁 S 밁

RESULT 8 BQ752001 LOCUS

δ 밁 S 밁 8 밁 δ 밁 Ś

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SOURCE
ORGANISM
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Best Local Similarity
                                                                                                                                                                                               Samac, D.A., Dickman, M., Town, C.D., Var
Cheung, F. and Fraser, C.M.
BSTs from mycelia of Colletotrichum tr
Unpublished (2002)
Other ESTs: EST611577
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164
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BQ751015
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EST631578
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Colletotrichum trifolii
Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
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TIGR sequence name: MTSAB07TV
www.medicago.org
Seq primer: (gtA AtA CgA CtC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ751015.1
EST.
                                                                               Email: debbys@puccini.crl.umn
TIGR sequence name: MTSAB07TV
                                                                                                                             Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                          495 Borlaug Hall, 1991 Upper Buford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTCGAGCGTCATTTCAACCCTCAAGCACC---GCTTGGCGTTGGGGG------
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                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 806)
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/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
RCORI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
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/lab_host="DH5alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSCT Colletotrichum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:21906420
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Pred. No. 5.6e-21;
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                            ACt AtA ggg
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                                                                    .edu
More information
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trifolii cDNA clone pDSCT2-7, mRNA
                                                                                                                                                                                                                                                                                                                                                                          Van Aken, S., Utterback, T.,
                                                                                                                                                                          Circle,
                                                                                                                                                                                                                                                                                                                            trifolii race
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                              G
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                                                                               18
                                                                                                                                                                          Paul,
                                                                               available
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                                                                                                                                                                          MN 55108,
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ACCESSION
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BQ751484
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                                                                                                                         TITLE
                                                                                                                                                                AUTHORS
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                                                                       Samac,D.A., Dickman,M., Town,C.D., V
Cheung,F. and Fraser,C.M.
ESTs from mycelia of Colletotrichum
Unpublished (2002)
Other ESTs: EST632046
                  Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; Sordariomycetes incertae sedis; Phyllachoraceae; Colletotrichum.
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                                                                                                                                                                                                                                                        Colletotrichum trifolii
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EST632047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTAGTAACATACCACCTCGCACCGGGACCCGCAGGGCACTCCTGCCGTAAAACCCCCCCA
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                                                                                                                                                                              (bases 1 to 806)
    Borlaug Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: EcoRI; isolate: 2sp2; cDNA was prepared from polyA+enriched RNA The cDNA was ligated into Lambda gtll from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab_host="DH5alpha"
                                                                                                                                                                                                                                                                                                                                                                             DSCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:5466"
/clone="pDSCT2-7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Colletotrichum trifolii"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="mycelia"
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                                                                                                                                                   Dickman, M., Town, C.D., Van Aken, S., Utterback, T.,
                                                                                                                                                                                                                                                                                                                   GI:21906889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.7%;
77.6%;
                                                                                                                                                                                                                                                                                                                                                                    806 bp mRNA linear EST 18-JU Colletotrichum trifolii cDNA clone pDSCT5-48,
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1991 Upper Buford Circle,
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Pred. No. 5.9e-21;
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                                                                                                                    trifolii race 1
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  St. Paul,
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MN 55108,
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USA
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Best Local
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                                                                                                                                                   sequence.
BQ751971
BQ751971.1
BST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225;
                                                                                                            Colletotrichum trifolii
Colletotrichum trifolii
              Samac, D.A., Dickman, M.,
                            Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.

1 (bases 1 to 745)
                                                                                                                                                                                                                                 BQ751971
EST632534
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Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TIGR sequence name: WTSAE48TV More
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTAGTAGC-TAACACCTCGCAACTGGA-GAGCGGCGGCGGCCACGCCGTAAAACACCCCAA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTGCGGGCACAACGCCGTCCCCCAAATACAGTGGCGGTCCCGC-CGCAGCTTCCATTG
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inoculation) grown in liquid
containing 2%glucose)."
/lab_host="DH5alpha"
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/mol_type="mRNA"
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77.6%;
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Pred. No. 5.9e-21;
0; Mismatches 43
            Town, C.D.,
                                                                                                                                                                                                                             bp mRNA
n trifolii |
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d culture (cutin
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            Aken, S.,
                                                                                                                                                                                                                             CDNA
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A clone
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            Utterback, T.,
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minimal medium
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St.

Paul, MN 55108, USA

Utterback, T.,

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KEYWORDS
SOURCE
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Best Local Similarity
    ORGANISM
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  Colletotrichum Colletotrichum
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EST631962 DSCT Colletotrichum
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Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAIO3TV More information is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle,
                                                                    BQ751399.1
                                                                                                          sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  www.medicago.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002
                                                                                                                                                                                                                                                                                         CTTCT--GAATGTTGACCTCGAATCAGGTAGGAATACCCGGCTGAACTTAA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTGCGGGCACAACGCCGTCCCCAAATACAGTGGCGGTCCCGC-CGCAGCTTCCATTG
                                                                                                                                                                                                                                                                                                                                                    CGTAGTAACATACCACCTCGCACCGGGACCCGCAGGGCACTCCTGCCGTAAAACCCCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTCGAGCGTCATTTCAACCCTCAAGCACC---GCTTGGCGTTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTGATTCATCGAATCTTTGAACGCACATTGCGCCCGCCAGCATTCTGGCGGCATGCCT
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                                                                                                                                                                                                                                                                ATTTTTACAAGGTTGACCTCGGATCAGGTAGGAATACCCGCTGAACTTAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                        -CTTCCACGGCTGACGTGGGCCCTCAAAGACAGTGGCGGACCCTCGCGGAGCCTCCTTTG
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/clone lib="DSCT"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
recombinants."
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inoculation) grown in liquid culture (cutin minimal medium
containing 2%glucose)."
/lab_host="DH5alpha"
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Location/Qualifiers
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                                                                    GI:21906804
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77.2%;
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Pred. No. 1.5e-20;
0; Mismatches 44
                                                                                                                               758 bp mRNA linear EST 18-JUL-2002 chum trifolii cDNA clone pDSCT4-95, mRNA
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Other ESTs: EST631961
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
  BM870292
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TIGR sequence name: MTSAD95TV More information
www.medicago.org
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Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Ut Cheung,F. and Fraser,C.M.
ESTs from mycelia of Colletotrichum trifolii race
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Fax: 651 649 5058
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/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK+; Site_1: EcoRI; Isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
recombinants."
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/tissue_type="mycella"
/tissue_type="mycella"
/dev_stage="Young, actively growing mycella (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab_host="DH5alpha"
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77.2%;
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Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mgns009xJ23f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgns009xJ23 5', mRNA sequence.
BM870292
BM870292.2 GI:30404719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromatogram file of this sequence is available, see contact person; Best nr hit (April. 22, 2003) gb|AAL79278.1| unknown [Saccharomyces cerevisiae] 79 le-14
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[ (bases 1 to 169)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Magnaporthe
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TCGG 162
                                                                                   TIGCGCCCGCCGGTATTCCGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                                                                                                                            AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
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979 845 6483
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/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Nitrogen starvation library. Cells were inoculated into
minimal medium and grown for two days with shaking (150
rpm) at room temperature. Culture was harvested, blended,
inoculated into minimal medium as above for 24 h. Cells
were harvested, washed with water and inoculated into
minimal medium base lacking nitrogen source for 6 h.
Sequences were processed by one of two methods. Where a
full-length alignment to the M. grisea genome sequence was
available, the EST sequence was trimed according to the
alignment, otherwise sequence quality was assessed using
phredPhrap version 991019 and trimmed according to phd
files (0.05) and for vector seqs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="mgns009xJ23"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
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95.2%;
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                                                                                                                                                                                                                                                                                               Score 114.4;
Pred. No. 1.
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Cheung,F. and Fraser,C.M.
ESTs from mycelia of Colletotrichum trifolii race 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             495 Borlaug Hall, 1991 Upper Buford Circle,
Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
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Other_ESTs: EST632698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.
                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAJZ3TV More information
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BQ752136
                                     CGGGCACAACGCCGTCCCCCAAATACAGTGGCGGTCCCGC-CGCAGCTTCCATTGCGTAG 218
CACGGCTGACGTGGGCCCTCAAAGACAGTGGCGGACCCTCGCGGAGCCTCCTTTGCGTAG
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/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DHSalpha which
                                                                                                                                                                                                                                                                                                                                             were plated onto medium with X-gal recombinants."
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inoculation) grown in liquid culture (cutin minimal medium
containing 2%glucose)."
/lab_host="DH5alpha"
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/mol_type="mRNA"
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76.8%;
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Pred. No. 3.6e-19;
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ą	Db	Ş	Query Match Best Local Si Matches 218,	ORIGIN		FEATURES source	TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 15 BQ751027 LOCUS DEFINITION	B &	g Q
100 AGCGTCATTACAACCCTCAGGCCCCCGGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTG 159	5 ATTTTCGAATCTTTGAACGCACATTGCGCCCGCCAGCATTCTGGCGGCATGCCTGTTCG 64	40 ATCATCGAATCTTTGAACGCACATTGCGCCCGCCCAGTATTCTGGCGGGCATGCCTGTTCG 99	ch 34.2%; Score 109; DB 13; Length 743; al Similarity 76.5%; Pred. No. 9.5e-19; 218; Conservative 0; Mismatches 45; Indels 22; Gaps 6;	/clone="pubscrp2-20" /clone="pubscrp2-20" /tissue_type="mycelia" /tissue_type="mycelia" /dev_stage="Young, actively growing mycelia (3 days after /dev_stage="Young, actively growing mycelia (noculation) grown in liquid culture (cutin minimal medium containing 2 fglucose)." /lab host="phisalpha" /clone="bis="DSCT" /clone="bis="DSCT" /note="vector: pBluescript Sk+; Site 1: EcoRI; Site 2: /coRI; isolate: 2sp2; cDNA was prepared from polyA+ enriched RNA The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript Sk+. Aliquots of the ligation were used to transform E. coli DHSalpha which were plated onto medium with X-gal for selection of	rganism="Colletot ol_type="mRNA" train="race 1" h xref="taxon:546	Seq primer I 1	Cheung, F. and Fraser, C.M. ESTs from mycelia of Colletotrichum trifolii race 1 Unpublished (2002) Other_ESTs: EST631589	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum. 1 (bases 1 to 743) Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T.,	sequence. BQ751027.1 GI:21906432 EST. Colletotrichum trifolii Colletotrichum trifolii	BQ751027 743 bp mRNA linear EST 18-JUL-2002 EST631590 DSCT Colletotrichum trifolii cDNA clone pDSCT2-20, mRNA	277GAATGTTGACCTCGAATCAGGTAGGAATACCCGCTGAACTTAA 319 	219 TAGC-TAACACCTCGCAACTGGA-GAGCGGCGGCGGCGACGCCGTAAAACACCCCAACTTCT 276

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Db 65 AGCGTCATTTCAACCCTCAAACACCT.--GCTTGGCGTTGGGG------CTTC 107

Qy 160 CGGGCACAACGCCGTCCCCCAAATACACTGGCGGTCCCGC-CGCAGCTTCCCATTGCGTAG 218

Db 108 CACGGCTGACGTGGCCTCCAAAGACACGTGGCGGACCCTCGCAGACCTTCC 276

Qy 219 TAGC-TAACACCTCGCAACTGGA-GAGCGGGCGACGCCGTAAAACACCCCCAACTTCT 276

Db 168 TAACATACCACCTCGCAACTGGA-GAGCGGGGCACGCCGTAAAACACCCCCAACTTCT 227

Qy 277 --GAAGACCTCGGAACAGGACCGGAACGGAACTCCTGCCCAACTTTT 227

Qy 277 --GAAGACTTGAATCAGGTAGGAATACCCGCCGAACTTAA 319

Db 228 TACAAGGTTGACCTCGGATCAGGTAGGAATACCCGCTGAACTTAA 272
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Search completed: October 1, 2004, 08:01:33 Job time : 4475.33 secs

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Maximum
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Pred. No. 18 the number of results predicted by chance to have

TITLE JOURNAL

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS KEYWORDS SOURCE ORGANISM RESULT 1 AR206400 LOCUS DEFINITION ACCESSION VERSION Result No. Unknown. Unclassified. 1 (bases 1 to 319) 1 (bases 1 to 319) Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.Soo. Nucleic acids for detecting Aspergillus species and other filamentous fungi Patent: US 6372430-A 6 16-APR-2002; Sequence AR206400 Unknown. AR206400.1 AR206400 Match 100.0 100.0 100.0 99.4 99.4 99.5 91.5 87.5 87.5 87.5 9 σ Length from patent US GI:21504990 BB AR206400 AR206401 AR217921 AR7429048 AR74290467 AR74290467 AR74290467 AR74290467 AR74290467 AR74290467 AR74290461 AR74290 ALIGNMENTS 6372430. ģ DNA linear AF150479 AF150480 AF150454 AF150455 AF150456 AF150457 AF150469 AF150469 AF150470 AF150470 AF150475 AF111061 AY243054 AF150476 AF150449 AF150450 AF150451 AF150451 AF440567 AY2723332 AF132801 AF150460 AF1504661 AF1504661 AF1504663 AF1504663 AF1504664 AF150477 AF150478 AY429048 AY429053 Description AR206400 PAT 20-JUN-2002 Neocosmospo Ascomycet Nectria h Nucctria and Nectria by Schaetomiu Chaetomiu Chaetomiu Nectria by Schaetomiu Nectria by Neocosmos Fusarium Sequence Nucleic a Fusarium

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ILL PATENT, UP 2001525665-A 6 11-DEC-2001;
PATENT UP 2001525665-A 6 11-DEC-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O
CENTERS FOR JAPAN FORACE SEED ASSOCIATION DISEASE CONTROL AND
PREVENTION TECHNOLOGY TRANSFER OFFICE
OS FUSATIUM SOLANI
OF 2001525665-A/6
PD 11-DEC-2001
PF 01-MAY-1998 JP 1998548275
PF 02-MAY-1998 JP 1998548275
PF 01-MAY-1998 JP 1998548275
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CHOI
STANDEDGES: Single;
CC Strandedness: Single;
CC Topology: Linear;
FH Key Linear;
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                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 319)
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.
Nucleic acids for detecting Aspergillus species and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids for detecting Aspergillus species and other sparsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        μ
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Fusarium solani
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                                                                 Location/Qualifiers.
/organism="Fusarium solani"
/mol_type="genomic DNA"
/db_xref="taxon:169388"
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 Query Match
Best Local Similarity
Matches 319; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF117921 319 bp DNA linear Placetria haematococca 5.8S ribosomal RNA gene, partial internal transcribed spacer 2, complete sequence; and RNA gene, partial sequence.
                                                                                                                                                                                                                                                                    Submitted (09-SEP-1998)
                                                                                                                                                                                                                                                                                 Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998) (bases 1 to 319) (Choi.J.S., Westerman, J.M. and Morrison, C.J. Direct Submission
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (Dases 1 to 319)
Choi, J.S., Westerman, J.M. and Morrison, C.J.
Rapid differentiation of filamentous fungi using species-specific
                                                                                                                                                                                                                                                                                                                                                                                                                               Fusarium solani
Fusarium solani
                                                                                                                                                                                                                                                                                                                                        DNA probes
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100.0%; ilarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                      USA
                                                                                                                                                                       /organism="Fusarium solani"
/mol_type="genomic DNA"
/db_xref="taxon:169388"
                                                                                                   /product="internal transcribed spacer
/note="ITS2"
                                                                                                                                   /product="5.88
160. .272
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                        'product="28S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Fusarium solani"
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Score 319; DB 8;
Pred. No. 2e-165;
; Mismatches 0;
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Pred. No. 2e-165;
                                                                                                                                                ribosomal
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                                                                                                                                                                                                                                                                                                                                                                                 Aggarwal,R., Renu,S. and Singh,D.V. Direct Submission Submitted (07-OCT-2003) Division of Plant Road, New Delhi, Delhi 110012, India
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV429048 559 bp DNA linear PLN 30-NOV-: Chaetcomium globosum isolate Cg1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 559)
Aggarwal, R., Renu, S. an
Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chaetomium globosum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chaetomium globosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chaetomium globosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATACCCGCTGAACTTAA 319
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                 TTGCGCCCGCCAGTATTCTGGCGGGCATGCCCTGTTCGAGCGTCATTACAACCCTCAGGCC
                                                                                  AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCTTTGAACGCACA
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                                                                AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 559)
                                                                                                                               99.4%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                /note="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
                                                                                                                                                                                                                                                                                          'mol type="genomic DNA"
'isolate="Cg1"
'dh vr>f ".
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of full length ITS
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Pred. No. 2.5e-164;
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Aggarwal, R., Renu, S. and Singh, D.V.
Nucleotide sequence of full length ITS
Chaetomium globosum
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (07-OCT-2003) Division of Plant Road, New Delhi, Delhi 110012, India
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Aggarwal,R., Renu,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                 TACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAGA 242
                                                                                    CCCGGGCCTGGCGTTGGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCCAAA
                                                                                                                                 TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGCC
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spacer 1, 5.8S ribosomal RNA,
2, and 28S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Chaetomium globosum"
/mol_type="genomic DNA"
/isolate="Cg6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-2003) Agronomy of Queensland, Warrego Highway, ( Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 576)
Scott, P.T., Martin, H.L., Boreel, S.M., Wearing, A.H. and Maclean, D.J. Isolation and characterization of Nectria haematoccoca from table beet grown in the Lockyer Valley, Queensland, Australia
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AY310442
Nectria haematococca 18S ribosomal RNA gene, partial sequence, internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence, and 28S ribosomal RNA gene, partial sequence.
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Nectria haematococca
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AY310442.1 GI:32264972
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 GCGGCGCGCCACGCCGTAAAACACCCAACTTCTGAATGTTGACCTCGAATCAGGTAGGA
                                          TACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAGA
                                                            TACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAAGA
                                                                                               CCCGGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCAAA
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519. .>576
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/mol_type="genomic DNA"
/db xrefe"taxon:140110"
/country="Australia: Lockyer Val
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100.0%; Pr
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Gatton, QLD 4343,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGGCGCGGCCACGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGGA
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larity 100.0%; 1
Conservative 0;
                                                                                                                                                                                                                                                                                                                                        /product="internal transcribed
/note="ITS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Fusarium"
/mol_type="genomic I
/strain="ATCC62877"
                                                                                                                                                                                                                                                                                                               'product="28S ribosomal RNA'
                                                                                                                                                                                                                                                                                                                                                                                                                        product="internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:169388"
                                                                                                                                                                                                                                                                                                                                                                                 product="5.8S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                         note="ITS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="ATCC:62877"
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                                                                                                                                                                                                                                          Score 308; DB;; Pred. No. 2.5;
0; Mismatches
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202 AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
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(Dases 1 to 509)
(Dases 1 to 509)
(Pages 2 to
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Iwen, P.C., Henry, T. and Hinrichs, S.H.

Sequence analysis of the internal transcribed spacer Fusarium species most commonly associated with human
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
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GCGGCGCGGCCACGCCGTAAAACACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGGA 302
                                                                                                                 TACAGTGGCGGTCCCGCCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAGA
                                                                                                                                                                                                              TACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAGA
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LOCUS
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    complete
AF150466
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                          AF150466 100 AF150466 PDNA linear PLN (Nectria haematococca strain SUF209 internal transcribed spacer 5.85 ribosomal RNA gene, and internal transcribed spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AY226096 298 bp DNA linear PLN 27-MAR-2003 Nectria haematococca 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal
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1. (bases 1 to 298)
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Nectria haematococca
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                                                                                                                                      CCAACTTCTGAATGTTGACCTCGAATCAGGTAGGAATACCCGCTGAACTTAA 319
                                                                                                                                                                                             CCATTGCGTAGTAGCTAACACCTCGCAACTGGAGAGCGGCGGCGGCCGCCGTAAAACAC
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                                                                                                                                                                                                                                                GGAAGCCCCCTGCGGGCACAACGCCGTCCCCCAAATACAGTGGCGGTCCCGCCGCAGCTT
                                                                                                                        CCAACTTCTGAATGTTGACCTCGAATCAGGTAGGAATACCCGCTGAACTTAA 292
                                                                                                                                                                            CCATTGCGTAGTAGCTAACACCTCGCAACTGGAGAGCGGCGGCGGCCACGCCGTAAAACAC
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                sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="5.8S ribosomal RNA"
133. .245
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<1. .132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Nectria haematococca"
/mol_type="genomic_DNA"
/strain="260499/24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="28S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product="internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                          91.5%; Score 292; DB 8; Lo
100.0%; Pred. No. 1.9e-150;
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Nectria haematococca strain SUF210
5.85 ribosomal RNA gene, and intern
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Suga, H., Hasegawa, T., Mitsui, H., Kageyama, K. and Phylogenetic analysis of phytopathogenic fungus, based on the rDNA-ITS region
                                                                                                                     complete sequence. AF150467 AF150467.1 GI:765
                                                                              Nectria haematococca
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                                                                                                                       GI:7650165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _xref="taxon:140110"
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 480)
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Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suga, H., Hasegawa, T., Mitsui, H., Kageyama, K. and Hyakumachi, M. Phylogenetic analysis of phytopathogenic fungus, Fusarium sola based on the rDNA-ITS region
Mycol. Res. 104 (10), 1175-1183 (2000)
2 (bases 1 to 480)
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/mol_type="genomic DNA"
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Pred. No. 3.1e-143;
                                                                                                                                                                                                                                                                                       internal transcribed
                                                                                                                                                                                                                                                                                                     UNA linear PLN 05-JAN-2001 internal transcribed spacer 1,
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Best Local S
Matches 279
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          Direct Submission
Direct Submission
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279;
                                                                                           from tomato plants
Can. J. Bot. 80 (3), 271-279 (2002)
2 (bases 1 to 480)
Bao,J.R., Fravel,D.R. and Lazarovits,G.
                                                                                                                                                          Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
                                                                                                                                                                                  Bao, J.R., Fravel, D.R., O'Neill, N.R., Lazarovits, G. and van Berkum, P.
                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 480)
                                                                                                                                                                                                                                                                                                                                                         AF440567

Nectria haematococca isolate
5.85 ribosomal RNA gene, and
                                                                                                                                                                                                                                                              Fusarium solani
Fusarium solani
                                                                                                                                                                                                                                                                                                              AF440567.1 GI:18034435
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                                                                                                                                                                                                                                                                                                                                               complete sequence.
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Direct Submission
Submitted (12-MAY-1999) Molecular Genetics
University, Gifu 501-1112, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suga,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycol. Res. 104 (10), 1175-1183 (2000)
2 (bases 1 to 480)
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organism="Fusarium solani"/
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309. .480
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/mol_type="genomic DNA"
/strain="SUF210"
/db_xref="taxon:140110"
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internal transcribed spacer 2,
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                                                                                                                                                                                                                                                      1 (bases 1 to 569)

Aggarwal, R., Renu, S. and Singh, D.V.

Nucleotide sequence of full-length Chaetomium globosum

Onublished
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                                                                                                                                                                      2 (bases 1 to 569)
Aggarwal,R., Renu,S. and Singh,D.V.
Direct Submission
Submitted (07-OCT-2003) Division of Plant Pathology, IARI,
Road, New Delhi, Delhi 110012, India
                                                                                                                                                                                                                                                                                                                                     Chaetomium globosum
Chaetomium globosum
Chaetomium globosum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AY429049 569 bp DNA linear PLN 30-NOV-: Chaetomium globosum isolate Cg2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
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          /note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed space, and 28S ribosomal RNA"
                                                                                                                                                      Delhi, Delhi 110012, India
Location/Qualifiers
                                                                       /db_xref="taxon:38033"
                                                                                            /organism="Chaetomium globosum'
/mol_type="genomic DNA"
/isolate="Cg2"
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/isolate="CS-1"
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Pred. No. 3.1e-143;
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Query Match

83.4%;

Score 266;

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                                                                                                                                                                                                                                                                                                  Unpublished

(bases 1 to 501)

(bases 1 to 501)

Roose-Amsaleg,C., Brygoo,Y. and Harry,M.

Direct Submission

Submitted (09-APR-2003) UFR Sciences Universite Paris 12,

Submitted (09-APR-2003) UFR Sciences Universite Paris 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uncultured ascomycete clone T7Å6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 501)
Roose Amsaleg,C., Brygoo,Y. and Harry,M.
Marked discrepancy between fungal divers
termitaries and tropical soils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uncultured ascomycete
Eukaryota; Fungi; Ascomycota; environmental
                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Conservative
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/db_xref="taxon:175243"
                                                                                                                    spacer
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                         /product="5.8S ribosomal RNA"
293. .>501
                                                                                                                                                                                                                                /organism="uncultured ascomycete"
/mol_type="genomic DNA"
/isolation_source="termitarie of Cubitermes
                                             /note="contains
ribosomal RNA"
                                                                                                                                   /note="contains 18S ribosomal RNA
                                                                                                                                                             /country="Gabon:
                                                                                                                                                                                            clone="T7A6"
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AF132801.1
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Submitted (03-MAR-1999) Plant Pathology,
Room 351 Bessey Hall, Ames, IA 50011, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusarium solani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycete
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 478)
Harrington, T.C., Steimel, J.P., Workneh, F. and Yang, X.B.
Molecular Identification of Fungi Associated with Vascular
Discoloration of Soybean in the North Central United States
Plant Dis. 84 (1), 83-89 (2000)

2 (bases 1 to 478)
Harrington, T.C., Steimel, J.P., Workneh, F. and Yang, X.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF132801 478 bp DNA linear PLN 20-JAN-2000 Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal RNA, and internal transcribed spacer 2, complete sequence.
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                                                                              Similarity
               AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAGA
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                                                                 Conservative
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                                                                                                                                               /product="internal transcribed spacer
/note="ITS2"
                                                                                                                                                                           product="5.8S
107. .478
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                                                                                                                                                                                                                                                                                                             specific_host="Glycine max"
db_xref="taxon:169388"
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                                                                                                                                                                                                                                                                                                                                                                              organism="Fusarium solani"
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                                                                                                                                                                                                                                                                            country="USA:
                                                                                                                                                                                                                                                                                             tissue_type="mycelium"
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                                                                             DB 8;
1.7e-75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                      Query Match 49.2%; Score 157; DB 8; L
Best Local Similarity 100.0%; Pred. No. 1.7e-75;
Matches 157; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                         201 AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
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API50459
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Rectria haematococca

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 478)

Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.

Phylogenetic analysis of phytopathogenic fungus, Fusarium solani

based on the rDNA-TTS region

Mycol. Res. 104 (10), 1175-1183 (2000)

2 (bases 1 to 478)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu University, Gifu 501-1112, Japan Location/Qualifiers
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                                                                                                                                      TIGCGCCCGCCAGTATICIGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGGCC 320
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                                                                                                                                                                                                                                                                                                                                                            /product="5.8S ribosomal RNA"
308. .478
/product="internal transcribed spacer 2"
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/mol_type="genomic_DNA"
/strain="K-1"
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/note="anamorph: Fusarium solani"
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                   2004, 09:56:21
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Aat05394	Aba94563	Aav62506	Aat05399	Aba01153	Aba94562	Aav62505	Aat05398	Ada27221	Aaz22436	Aaf75170	Aaf75169	Aba94560	Aba94561	Aba94564	Aba94559	Aav70870	Aav70871	Aaz91725	Abv78724	Aav59009	Aat05403
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ALIGNMENTS

Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; M. racemosus; M. plumbeus; M. indiccus; A. fumigatus; M. circinalloides f. circinelloides; Rhizopus oryzae; R. microsporus; R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum; 26-FEB-1999 AAV70850; Penicillium notatum; Sporothrix schenkii; filamentous fungus; ss Internal transcribed spacer 2 (ITS2) and adjacent regions. AAV70850 standard; (first entry) DNA; 319 ₽P

~ 4 ~ W	Fusarium solani. WO9850584-A2.
	12-NOV-1998.
	01-MAY-1998;
	02-MAY-1997;
	(USSH) US DEPT HEALTH & HUMAN SERVICES.
	Morrison CJ,

New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothr species. Sporothrix

WPI; 1999-034737/03.

Claim 1; Page 12; 45pp; English.

The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species. Specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,

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RESULT 2
AAA72783
ID AAA7
XX AAA7
AC AAA7
AC AAA7
XX Blac
XX Blac
XX Fusa
XX Fusa
XX WC20
XX Fusa
YX WC20
XX WC1;
XX WC1;
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Best Local
             Nucleic acid based assay and kit for detection of Alternaria contamination in food products involves analyzing the sample product for nucleic acid sequences unique to Alternaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeum M. indicus, M. circinilloides f. circinelloides, Rhizopus oryzae, R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallesheria boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenkii. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi
                                                                       WPI; 2000-499381/44
                                                                                                                                                                     02-FEB-1999;
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                                                                                                                                                                                                                                                                                                              spot disease; brown spot disease; fungi; fruit vegetable;
crop; Alternaria; 5.8s rRNA; detection; ds.
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Matches 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ribosomal DNA, rDNA ITS region; internal transcribed spacer; ATCC 74469; HIV integrase inhibitor; steroid compound; human immunodeficency virus; acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex; symptomatic infection; asymptomatic infection; potential HIV exposure;
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14-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusarium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA61893;
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                                                                                                                                                                                                                                                                                                                                            SB,
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                                                                                                                                                                                                                                                                                                              Zink DL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MF6381 rDNA internal transcribed spacer
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100.0%; Pr/
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Pred. No. 1.9e-46;
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                                                                                                                                                                                                                                                                                                                                         Polishook JD;
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The invention relates to novel steroid compounds derived from soil fungus Fusarium sp. MF6381 (ATCC 74469) which act as inhibit integrase. The invention encompasses cultures of Fusarium The invention also relates to a composition comprising a compo

d from the ... as inhibitors of usarium sp. MF6381.

infection

steroid compounds are ection and AIDS.

VΙΗ

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Page 14; 113pp;

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Matches 107
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A novel method for the detection of plant pathogenic strains of fungi e.g. Septoria nodorum, S.tritici, Pseudocercosporella herpotrichoides, Mycosphaerella fijiensis, M.musicola or Fusacrium spp, involves the PCR amplification of sequences found in the internal transcribed region (ITS) of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93 and AAT05357-72. These primers are derived from the ITS sequences of
                                                                                                                                                                                                                                                                                                                       DNA encoding
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                                                                                                                                                                                                                       Page 54-55; 65pp;
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                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amplification products of the reactions using these primers can be used with the capture primers AAT05378-93 in colourimetric assays. The prime and ITS DNAs can be used for the detection of specific fungal pathogen
           DNA isolated from fungal RNA, seguence - used for detecting
                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                   Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen; Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant; Septoria avenae; Microdochicum nivale; Fusarium poae; Fusarium avenaceum; PCR; nucleic acid detection; ss.
                                           WPI; 1998-541745/46
                                                                                                                                           02-JUL-1997;
                                                                                                                                                                                      US5814453-A.
                                                                                                                                                                                                                                                                                                                                                                                                Fusarium culmorum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusarium culmorum PCR amplified ITS region consensus DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 504 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               these fungi (AAT05394-T05404 and AAQ94398) and are strain specific.
                                                                                     (NOVS ) NOVARTIS
                                                                                                          19-APR-1995;
15-OCT-1996;
                                                                                                                                                                29-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in monitoring disease development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                          95WO-US004712.
96US-00722187.
                                                                                                                                           97US-00887480
                                                                                                                                                                                                                                                               /*tag= c
/note= "5.8S
319. .472
                                                                                                                                                                                                                                473. .504
                                                                                                                                                                                                                                                                                                 162. .318
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                13. .161
                                                                                     FINANCE CORP
                                                                                                                                                                                                          note= "5'
                                                                                                                                                                                                                                         /*tag= d
/note= "ITS
                                                                                                                                                                                                                                                                                                         /*tag= b
/note= "ITS
                                                                                                                                                                                                                                                                                                                                        note= "3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 132 C; 113 G; 122 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504
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                                                                                                                                                                                                                                                                          rRNA
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Pred. No.
           and its internal transcribed spacer fungal pathogens in plant tissue.
                                                                                                                                                                                                        of large subunit rRNA gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                          small subunit rRNA
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Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This represents the consensus DNA sequence of the internal transcribed spacer (ITS) region that was PCR amplified from Fusarium culmorum isolates, R-5106, R-5126 and R-5146. The invention provides a DNA molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal pathogen, where the DNA molecule consists of an ITS sequence selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium moniliforme, Septoria avenae or Microdochicum nivale. A method for detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F. avenaceum and M. nivale isolates is also provided. The method comprises isolating DNA from a plant leaf infected with at least one of the above pathogens and amplifying parts of the ITS sequence of the pathogen(s) by PCR using specific primers from within these sequences. The pathogen(s) are detected by visualising the amplified part of the ITS sequence
                Wheat pathogen internal transcribed spacer sequences - used for primers for the species-specific polymerase chain reactiof the pathogens.
                                                                      WPI; 1998-593995/50
                                                                                                                                                         04-AUG-1997;
                                                                                                                                                                                   04-AUG-1997;
                                                                                                                                                                                                                 27-OCT-1998.
                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                Fusarium culmorum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     F. culmorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
06-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV59028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV59028 standard; DNA; 504 BP
                                                                                                                             (NOVS)
                                                                                                                                                                                                                                          US5827695-A
                                                                                                                                                                                                                                                                                                                                                                                                           Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen; fungal pathogen identification; infection identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGCGCCCCAGTATTCTGGCGGCATGCCTGTTCGAGCGTCATT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    internal transcribed spacer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                        97US-00905314.
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/note= "ITS1"
319. .472
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/note= "ITS2"
                                                                                                                             FINANCE CORP
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Pred. No. 1.9e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                           chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 504;
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                           as a basis
ion detection
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pathogens

Sequence 504 BP; 132 A; 133

C; 114

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Best Local :
                                                         The sequence is an internal transcribed spacer (ITS) region from Fusarium culmorum, isolate 62215. The ITS DNA sequences are useful for detecting Rhizoctonia cerealis, a fungal pathogen of wheat causing Sharp eyespot, for monitoring disease development in plant population, and for providing detailed information on the development and spread of specific pathogen races over extended geographical areas. The DNA sequences are specifically used as primers in PCR-based analysis for the identification of fungal pathotypes
                                                                                                                                                                                                                                                                                                                                                                              New internal transcribed spacer DNA sequences, useful for identifying fungal pathogen, particularly Rhizoctonia cerealis, and for monitoring disease development in plant population.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents an internal transcribed spacer (ITS) sequence of the invention. The primer pairs, based on the ITS sequences, are used for the PCR amplification detection of wheat Microdochium and Fusarium fungal pathogens, especially M. nivale, F. graminearum, F. culmorum, F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different strains of fungi show different symptoms during infection, which may or may not be due to infection. Barly identification of the strain causing the infection allows early, and more specific fungicidal treatment. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                           Disclosure; Page 31; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-442154/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JAN-2000; 2000US-00481293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-2001; 2001WO-EP000172.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusarium culmorum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sharp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Internal transcribed spacer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS08426 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAATGCGATAAGTAAIGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spacer; ITS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S; fungal pathogen; ss; wheat disease; identification; isolate 62215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Length 504;

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RESULT 9
ACC49999
ID ACC4
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ACC5000 ID ACC5
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Best Local :
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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods and primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beck
  ACC49999 standard; DNA; 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondria; fungal pathogen; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusarium spp.
                                                                                                                                                                                                                                                 228
                                                                                                                                                                                                                                                                                                                                                            107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274
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                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                              AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
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                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 138 A; 140 C; 119 G; 124 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                       33.5%; Score 107; DB 7; 100.0%; Pred. No. 1.9e-46; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 521;
                                                                                                                                                                                                                                                                                                                                                       Indels
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RESULT 10
ACC5002
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ACC ACC50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                   Gibberella moniliformis
                                                                                                                                                                                                                                                                                                                                   27-OCT-2003
14-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACC50002 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods and primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present
19-SEP-2002; 2002WO-US030311.
                                                                                                                                                                                                                       Mitochondria; fungal pathogen;
                                                                                                                                                                                                                                                                               Internal transcribed spacer RNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                        ACC50002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-2001; 2001US-00961755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Internal transcribed spacer RNA encoding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGCGCCCGCCAGTATTCTGGCGGCCATGCCTGTTCGAGCGTCATT
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                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 107; DB /; L
Pred. No. 1.9e-46;
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                                                                                                                                                                                                                                                                                  sequence
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RESULT 11
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Best Local (
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Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
                                                                                                             ;IGM
                                                                                                                                                      Beck JJ,
                                                                                                                                                                                                                                      24-SEP-2001; 2001US-00961755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondria; fungal pathogen;
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                                                                                                                                                                                                (SYGN )
                                                                                                                                                                                                                                                                                                                                                                                                               Fasarium proliferatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Internal transcribed spacer RNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACC50001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACC50001 standard; DNA; 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-SEP-2001; 2001US-00961755.
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                                                                                                           2003-363229/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107;
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                                                                                                                                                                                              SYNGENTA PARTICIPATIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGCGCCCCAGTATTCTGGCGGCATGCCTGTTCGAGCGTCATT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 39; 44pp; English.
                                                                                                                                                 Barnett CJ;
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100.0%;
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                                                                                                                                                                                              ÄG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 522;
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밁 á 멂 Ş

Claim

5

Page 38-39;

44pp; English

DNA isolated from fungal RNA, sequence - used for detecting

and its internal transcribed spacer fungal pathogens in plant tissue.

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RASULT 12
AAV6293
AAV6293
AC AAV62
AC AAV62
AC AAV62
DT 17-OC
DT 17-DB
XX
Inter
KW Fusar
KW PCR;
CW PC
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15-OCT-1996;
                                                                                                                                                                                                                                                                         02-JUL-1997;
                                                                                                                                                                                                                                                                                                                       29-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                                                                                                                                                                                                                                                                                               US5814453-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen; Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant; Septoria avenae; Microdochicum nivale; Fusarium poae; Fusarium avenaceu
                                                                                                                                                          (NOVS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusarium moniliforme PCR amplified ITS
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17-DEC-1998
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96US-00722187.
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/note= "ITS
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/note= "5.8S rRNA
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/note= "ITS
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Pred. No. 1.9e-46;
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AAV59030
ID AAV59
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25-MAR-2003
06-JAN-1999
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Wheat pathogen internal transcribed spacer sequences - used as a basis for primers for the species-specific polymerase chain reaction detection
                                                                                     WPI; 1998-593995/50
                                                                                                                                                                                                                                                  04-AUG-1997;
                                                                                                                                                                                                                                                                                                        04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                              27-OCT-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen; fungal pathogen identification; infection identification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         545 BP; 148 A; 143 C; 125 G; 129 T; 0 U; 0 Other;
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/note= "ITS1"
336. .488
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RESULT 14
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ID AAV62
XX AAV62
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XX Inter
XX Fusar
XX
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Matches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents an internal transcribed spacer (ITS) sequence of the invention. The primer pairs, based on the ITS sequences, are used for the PCR amplification detection of wheat Microdochium and Fusarium fungal pathogens, especially M. nivale, F. graminearum, F. culmorum, F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different strains of fungi show different symptoms during infection, which may or may not be due to infection. Barly identification of the strain causing the infection allows early, and more specific fungicidal treatment. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PF field.)
                           19-APR-1995;
15-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusarium poae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant; Septoria avenae; Microdochicum nivale; Fusarium poae; Fusarium avenaceum;
                                                                                                         02-JUL-1997;
                                                                                                                                                          29-SEP-1998
                                                                                                                                                                                                             US5814453-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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107; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen; culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATT 108
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                           95WO-US004712
96US-00722187
                                                                                                         97US-00887480
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/note= "ITS
490. .546
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/note= "ITS
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/note= "5'
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/note= "3'
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/note= "5.8S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      546
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RESULT 15
AAV59007
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA isolated from fungal RNA, and its internal transcribed spacer sequence - used for detecting fungal pathogens in plant tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Col 87-88; 56pp; English.
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                             04-AUG-1997;
                                                           04-AUG-1997;
                                                                                       27-OCT-1998.
                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                      Fusarium
                                                                                                                                                                                                                                                                                                 Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen; fungal pathogen identification; infection identification; ss.
                                                                                                                                                                                                                                                                                                                                              F. poae internal transcribed spacer.
                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
06-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                         AAV59007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV59007 standard; DNA; 546 BP.
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                                                                                                                     US5827695-A.
 (NOVS ) NOVARTIS FINANCE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                      poae.
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(first entry)
                             97US-00905314.
                                                           97US-00905314.
                                                                                                                                                                             /*tag= a
/note= "ITS1"
338. .489
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                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                    note= "ITS2"
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100.0%; Prf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 546;
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Search completed: October Job time : 274.27 secs

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wheat pathogen internal transcribed spacer sequences - used as a basis for primers for the species-specific polymerase chain reaction detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beck
                                                                                                                                                                                                               Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Col 25-26; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-593995/50
                                                                                                                                                                                                                                                       correct PR field.)
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                                                                      230 AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
 290
                                    62
                                                                                                          N
                                ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATT
                                                                                             AAAATGCGATAAGTAATGTGAAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC 61
                                                                                                                                            33.5%; Scillarity 100.0%; P. Conservative 0;
                                                                                                                                            Score 107; DB z; L
Pred. No. 1.9e-46;
                                                                                                                                                                                 Length 546;
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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 2000000000
      Query
Match Length
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Gapop_60.0 , Gapext 60.0
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319
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Copyright (c) 1993 - 2004 Compugen Ltd.
    BB
US-09-423-233-6
US-08-905-314A-19
US-08-905-314A-19
US-08-905-314A-29
US-09-481-293-32
PCT-US95-04712-82
US-08-887-480-84
US-08-905-314A-22
US-08-652-127C-7
US-08-652-127C-7
US-08-652-127C-5
US-09-423-233-7
US-08-652-127C-5
US-09-423-233-26
US-08-905-314A-24
US-08-952-127C-9
US-08-652-127C-9
US-08-652-127C-9
US-09-423-233-7
US-09-423-233-26
US-09-423-233-26
US-09-423-233-26
US-09-635-747-40
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19, Appl
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301

GAATACCCGCTGAACTTAA 319

RESULT 2 US-08-887-480-82

. B	B &	D Q	Db Qy	D Q	g Q	Query Best Lo Matches	RESULT 1 US-09-423-2 ; Sequence ; Patent No ; GENERAL I ; APPLICAN, TITLE OF ; TITLE OF ; TITLE OF ; CURRENT ; CURRE		2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
301 GAATACCCGCTGAACTTAA	241 GAGCGGCGCGCC 241 GAGCGGCGCGGCC	181 AATACAGTGGCGGTCCC	121 cccccaaac 121 cccccaaac	61 CATTGCGCCC	1 GAAAATGCGJ 1 GAAAATGCGJ	y Match Local Similarity hes 319; Conservat	233-6 233-6 6, Applicat io. 6372430 INFORMATION: NT: The Gove PINVENTION: PINVENTION: PERENCE: 030 APPLICATION FILING DATE OF SEQ ID NO 10 6 10 6 11 319 10 6 233-6		68 221.3 68 221.3 68 221.3 68 221.3 68 221.3 68 221.3 68 221.3 68 221.3 68 221.3
TGAACTTA	GCCACGCC 	CGGTCCCGC	recerre	GCCAGTAT GCCAGTAT	NTAAGTAAT NTAAGTAAT	100.0% 100.0% /ative	JS/09 ht of leic leic leic leic leic leic leic leic		5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
A 319	CACGCCGTAAAACACCCAACTTCTGAATGTTGACCTCGAATCAGGTAG 	CGCAGCTTCCATTGCGTAGTAC 	CCCCCGGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGCCGTCCCCC 	CATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTACAACCCTCAGG	GAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGC 	; Score 319; DB 4; L; Pred. No. 2.5e-167; 0; Mismatches 0;	3 United States of for Detecting tous Fungi /423,233	ALIGNMENTS	PCT-US95-04712-5 US-08-233-608-6 US-08-887-480-6 US-08-722-187-6 PCT-US95-04712-6 US-08-233-608-1 US-08-233-608-1 US-08-727-1 US-09-481-293-30 PCT-US95-04712-1 US-08-98-887-480-85 US-08-986-727-5 US-08-986-727-1 US-08-986-727-1 US-08-986-727-1 US-08-986-727-1 US-08-986-727-1 US-08-986-727-1 US-08-986-727-1
	TTGACCTCGAATCAGGTAG 300	SCTAACACCTCGCAACTGGA 240	GCACAACGCCGTCCCCA 180	CGTCATTACAACCCTCAGG 120	CATCGAATCTTTGAACGCA 60	Length 319; Indels 0; Gaps 0;	f America as Aspergillus Species and		Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 35, Appli Sequence 25, Appli Sequence 3, Appli Sequence 4, Appli

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US-08-887-480-82
                           Query Match
Best Local Similarity
Matches 107; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atent No. 5814453
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                           OTHER INFORMATION: FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                          FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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STREET: 520 White
CITY: Tarrytown
                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature LOCATION: 1..12 OTHER INFORMATION: /note OTHER INFORMATION: rRNA
                                                                                                     OTHER INFORMATION:
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                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: 162.318
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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2 AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC 61
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520 White Plains Road
                              Conservative
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919-541-8689
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L ISOLATE: R-5106, R-5126, and R-5146
L ISOLATE: (consensus sequence)
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319..472
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473..504
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                        Detection of Fungal Pathogens Using the Polymerase Chain Reaction
                                                                                                   /note= "5' end of large subunit
rRNA gene"
                                                                                                                                                                                                                                      /note=
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rRNA gene"
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                                           Score 107;
Pred. No.
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                                         9.9e-50;
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US-08-905-314A-19
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Beck,
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COUNTRY: USA
ZIP: 20779-2257
ZIP: 20779-2257
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
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COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature LOCATION: 1..12
OTHER INFORMATION: /note OTHER INFORMATION: rRNA
 LOCATION: 473..504
OTHER INFORMATION:
OTHER INFORMATION:
                                  NAME/KEY: misc_feature LOCATION: 473..504
                                                                                        LOCATION: 319.7472
OTHER INFORMATION:
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LOCATION: 162..318
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OTHER INFORMATION:
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LOCATION: 13..161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                            LOCATION: 162..318
OTHER INFORMATION:
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T: 3054 Cornwallis Road
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusarium culmorum
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rRNA gene"
/note= "5'
rRNA gene"
                                                                                                                                                              /note=
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                                                                                        /note=
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211 AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC

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Patent No. 5955274
GENERAL INFORMATION:
                                                     Matches
                                                                     Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 04-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: WALSH, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using
TITLE OF INVENTION: Polymerase Chain Reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..504
OTHER INFORMATION: /note
OTHER INFORMATION: intes
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ADDRESSEE: Ciba-Geigy Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                   OLECULE TYPE:
                                                                                                                                                                                                                                                                 STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/233,608
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                                                                                                                                                                                                                                                                                                                   ENGTH:
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                                                                     Similarity
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AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
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                                                33.5%; Score 107; DB 2; 1 (larity 100.0%; Pred. No. 9.9e-50; Conservative 0; Mismatches 0;
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                                                                                                                                 /note= "DNA sequence
internal transcribed
(fculm.con)"
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                                                                                                                                                  spacer region of Fusarium culmorum
                                                                                                                                                                    for the
                                                                                 Length 504;
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                                                   Indels
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                                                  Gaps
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; Sequence 82, Application PC/TUS9504712
; GENERAL INFORMATION:
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US-09-481-293-32
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; Sequence 32, App....
No. 6485907
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SEQ ID NO 32
LENGTH: 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Beck, James
APPLICANT: Barnett, Jason
TITLE OF INVENTION: PCR-Based Detection of Rhizoctonia cerealis
TITLE REFERENCE: PB/5-31135P1
TITLE REFERENCE: PB/5-31135P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: PB/5-31135P1
CURRENT APPLICATION NUMBER: US/09/481,293
CURRENT FILING DATE: 2000-01-11
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Fusarium culmorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using
TITLE OF INVENTION: Polymerase Chain Reaction
                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                        ZIP: 10532
                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271
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                                                                                                                                                                                                                             Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 504;
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US-08-887-480-84
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Patent No. 5814453
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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                             FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PR
                                                                                                    TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Beck,
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SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using
TITLE OF INVENTION: Polymerase Chain Reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 9
MOLECULE TYPE:
DRIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 520
CTTY: Tarrytown
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                                                   TYPE: nucleic STRANDEDNESS:
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OTHER INFORMATION: /note= "DNA sequence for the OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum OTHER INFORMATION: (fculm.con)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                     TOPOLOGY:
                                                                                        LENGTH:
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STRANDEDNESS: sing
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                                                                  nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: No. 5814453artis Corporation 520 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                   linear
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1..504
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                  DNA (genomic)
                                                    single
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100.0%; Pred. No. 9.9e-50;
tive 0; Mismatches 0;
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                                                                                                                                                                                                CGC 1739/PCT/CIP
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APPLICATION NUMBER: US/08/905
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541.8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                              ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Beck, James J.
TITLE OF INVENTION: DETEC
TITLE OF INVENTION: USING
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
CLONE: pCRFMON1
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                                                                                                                                                                                                                                                                                                                                                   CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 489..545
OTHER INFORMATION: /note= "5'
OTHER INFORMATION: rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature LOCATION: 336..488
OTHER INFORMATION: /not
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OTHER INFORMATION: /note= "3'
OTHER INFORMATION: rRNA gene"
                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 31..178
OTHER INFORMATION: /no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Fusarium moniliforme INDIVIDUAL ISOLATE: 4551
                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 33.5%; So al Similarity 100.0%; I 107; Conservative 0;
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3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DETECTION OF WHEAT FUNGAL PATHOGENS USING THE POLYMERASE CHAIN REACTION
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                                                                                                                                                                 US/08/905,314A
                                              CGC 1944
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; Pred. No. 9.9e-50;
0; Mismatches 0;
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RESULT 9
US-08-887-480-96
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Sequence 96, App...
No. 5814453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 107; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Beck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/887,480 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 489.545
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
                                                                                                                                                                      STREET: 520 WILL
CITY: Tarrytown
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LOCATION:
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OTHER INFORMATION:
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LOCATION: 336..488
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                                                                                                                                                                                              E: No. 5814453artis Corporation 520 White Plains Road
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31..178
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rRNA gene"
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RESULT 10
US-08-905-314A-22
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                                               Sequence 22, Application US/08905314A
Patent No. 5827695
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF 1
TITLE OF INVENTION: USING THE POL-
                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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OTHER INFORMATION:
FEATURE:
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APPLICATION NUMBER: US 08/722,187
'FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: FEATURE:
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OTHER INFORMATION:
FEATURE:
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ORIGINAL SOURCE:
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LENGTH: 546 base pairs
                 CORRESPONDENCE
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OTHER INFORMATION: /note OTHER INFORMATION: rRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature LOCATION: 181..337
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LOCATION: 1.30
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No. 5827695artis Corporation Patent Department
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rRNA gene"
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3R: CGC 1739/PCT/CIP
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Pred. No. 9.9e-50;
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STREET: 3054 Co

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RESULT 11
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
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COMPUTER READABLE FORM:
COMPUTER READABLE Floppy disk
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INDIVIDUAL ISOLATE: sequence)
IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: 490..546
OTHER INFORMATION: /note= "5'
OTHER INFORMATION: rRNA gene"
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OTHER INFORMATION: /note OTHER INFORMATION: rRNA
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OTHER INFORMATION: /no
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OTHER INFORMATION: /no
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LOCATION: 181.337
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TOPOLOGY: li
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CLASSIFICATION: 435
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TYPE: nucleic acid
                                                   290
                                                                                                                  230 AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC 289
                                                                    62 ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATT 108
                                                                                                                                          2 AAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC 61
                                               ATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATT 336
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I ISOLATE: T-427, T-534, and T-756 (consensus
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100.0%; Prr
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rRNA gene"
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Pred. No.
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TOPOLOGY:
US-08-652-127C-7
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SEQ ID NO 1
LENGTH: 2293
TYPE: DNA
ORGANISM: Gibberella fujikuroi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09645073 Patent No. 6287800 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                               TELEFAX: (613) 232-58
INFORMATION FOR SEQ ID NO:
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CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,770
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PRIOR FILING DATE: 1999-
NUMBER OF SEQ ID NOS: 1
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APPLICANT: Galazzo, Jorge
TITLE OF INVENTION: Prod
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                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-D
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                   NAME: George A. Seaby
REGISTRATION NUMBER: 24
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/652,127C FILING DATE: May 23, 1996 CLASSIFICATION: 435
                               STRANDEDNESS:
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                                               nucleic acid
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              linear
                                                                                                                                 (613)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            George A. Seaby
                                                                                               ) 232-5831
) NO: 7:
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DETECTION OF PLANT
PATHOGEN FUNGI
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RESULT 14
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US-08-652-127C-6
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Sequence 5, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (613) 232-58: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Richard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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CITY: Ottawa
COUNTRY: Cana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: George A. Seaby
REGISTRATION NUMBER: 24
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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ADDRESSEE: Seaby & MacLean
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o. 5792611
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(613) 77 NO: 6:
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100.0%; Pred. No. 3.5e-49;
htive 0; Mismatches 0; Indels
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DETECTION OF PLANT
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                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus 9 TITLE OF INVENTION: Other Filamentous Fungi FILE REFERENCE: 03063-0341WP CURRENT APPLICATION NUMBER: US/09/423,233 CURRENT FILING DATE: 2000-06-27 NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09423233 Patent No. 6372430
                                                                         Matches
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                                                                                                             Query Match
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TELEPAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                 TYPE: DNA
ORGANISM: Fusarium moniliforme
                                                                                                                                                                                                      LENGTH: 310
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NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 185
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
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ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby & MacLean
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                                                                                           Local
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STRANDEDNESS: doub
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                     30 AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCGCCAGTATTCTGGCGGGGCA
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                                                                                         Similarity
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100.0%; Pr/
0;
                                                                                         Score 79; pred. No.
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                                                                         Mismatches
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                                                                                         DB 4; Le 3.4e-34;
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유 성 Search completed: October 1, 2004, 11:12:56 Job time : 53.744 secs 90 TGCCTGTTCGAGCGTCATT 108
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Page 8

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Minimum
Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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       107
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

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15: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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Match
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Gapop 60.0 , Gapext 60.0
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       5 US-10-046-955-6
0 US-09-961-755A-5
0 US-09-961-755A-8
0 US-09-961-755A-7
5 US-10-046-955-27
5 US-10-046-955-26
US-09-961-663-14
US-09-961-663-16
US-09-961-663-16
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Million cell updates/sec
Sequence 6, Appli
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Sequence 27, Appli
Sequence 27, Appl
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Sequence 15, Appl
Sequence 15, Appl
Sequence 16, Appl
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Sequence 17, Appl
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US-10-156-761-4030 US-10-156-761-1 US-10-424-599-8721 US-10-358-929A-3	US-10-046-955-24 US-09-766-173C-11 US-10-046-955-28 US-10-046-955-51 US-10-083-357-356	US-10-046-955-29 US-10-046-955-4 US-10-046-955-2 US-10-046-955-3 US-10-046-955-3 US-10-083-357-360 US-10-083-357-355	-10-083-357- -10-083-357- -10-083-357- -10-083-359- -10-358-929A -10-358-929A	US-09-961-663-18 US-09-766-173C-5 US-09-766-173C-4 US-10-121-740-4 US-10-623-432-4 US-10-121-740-2 US-10-623-432-2 US-10-623-432-2 US-10-623-655-5 US-10-046-955-5 US-10-046-955-5 US-10-046-955-5
Sequence 4030, Ap Sequence 1, Appli Sequence 8721, Ap Sequence 3, Appli	—	36, 249	372 72, 71, 2,	Sequence 18, Appli Sequence 5, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 25, Appli Sequence 1, Appli

ALIGNMENTS

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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 6
LENGTH: 319
TYPE: DNA
ORGANISM: Fusarium solani
US-10-046-955-6
                                                                                                                                                                                                                                                      APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Asg
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCES: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US/9/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR APPLICATION NUMBER: US/98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR FILING DATE: 1998-05-02
NUMBER: OF SEQ ID NOS: 61
NUMBER: OF SEQ ID NOS: 61
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US-10-046-955-6
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Publication No. US20030129600A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for DistaPPLICANT: Control and Prevention
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
     Matches
                                Query Match
Best Local
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     Local Similarity
les 319; Conserv
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100.0%; Score 319; DB 15; llarity 100.0%; Pred. No. 3.3e-174; Conservative 0; Mismatches 0;
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     Gaps
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US-09-961-755A-6
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                                                                                                                             GENERAL INFORMATION:
APPLICANT: Beck, Jim
APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 60055
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CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
                   SOFTWARE: PatentIn version 3.0 SEQ ID NO 5 LENGTH: 522
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Best Local S
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                                                                       CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
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APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Fugarium Species infecting Corn Using the
TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 60055
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TYPE: DNA
ORGANISM: Gibberella zeae
TYPE: DNA
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les 107; Conserv
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RESULT 5
US-09-961-755A-7
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US-09-961-755A-8
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                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
SOPTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 534
TYPE: DNA
ORGANISM: Fusarium proliferatum
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CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 522
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APPLICANT: Beck, Jim
APPLICANT
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Query Match 33.5%; Score 107; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.8e-51;
Matches 107; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 107; Conservative
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the TITLE OF INVENTION: Polymerase Chain Reaction FILE REFERENCE: 60055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Beck, Jim APPLICANT: Barnett, Jason
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                                                                          Length 534;
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; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-10-046-955-7
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                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/10046955 Publication No. US20030129600A1 GENERAL INFORMATION:
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Publication No. US20030129600A1
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APPLICANT:
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      PRIOR
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                                                               APPLICANT: Aidorevich, Liliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
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PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
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APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
FULL REPERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
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NT FILING DATE: 2002-06-04
APPLICATION NUMBER: US 09/423,233
FILING DATE: 2000-06-27
APPLICATION NUMBER: PCT/US98/08926
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100.0%; Pred. No. 4.7
tive 0; Mismatches
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RESULT 9

US-09-961-663-14

Sequence 14, Application US/09961663 Patent No. US20020115084A1 GENERAL INFORMATION:

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; TYPE: DNA
; ORGANISM: Scedosporium apiospermum
US-10-046-955-26
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US-10-046-955-26
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                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR PILING DATE: 1998-05-02
PRIOR FILING DATE: 1997-05-02
PRIOR FILING DATE: 1997-05-02
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 6395-62064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species
TITLE OF INVENTION: Other Filamentous Fungi
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                                                                                                                                                            Local Similarity
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                             TTGCGCCCG 71
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Trácaccca 70
                                                                    ANATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
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                                                                                                                                         Conservative
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; Pred. No. 2.9e-29;
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TITLE OF INVENTION: Detection of Mycosphaerella Using the Pol-
TITLE OF INVENTION: Reaction
FILE REFERENCE: PB/S-31382A
CURRENT APPLICATION NUMBER: US/09/961,663
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 377
TYPE: DNA
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US-09-961-663-15
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SEQ ID NO 14
LENGTH: 377
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/961,663
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Barnett, Jason APPLICANT: Beck, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Barnett,
APPLICANT: Beck, J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: (1) . (377)
COTHER INFORMATION: Truncated DNA sequence for the Internal OTHER INFORMATION: Transcribed Spacer of a fungus amplified from OTHER INFORMATION: banana sample "Capesterre-babin 2".
                                                                                                                                                                                                                   FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(377)

OTHER INFORMATION: Transcribed DNA sequence for the Internal

OTHER INFORMATION: Transcribed Spacer of fungus amplified from l

OTHER INFORMATION: sample "Matouba bas 3"
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ORGANISM: Mycosphaerella
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                                            91 AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA 150
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                                                                     3 AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTTGAACGCACA 62
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      TTGCGCCC 70
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                                                                                                                              ilarity 100.0%;
Conservative (
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                                                                                                                                                 21.3%; Score 68; DB 9; L
100.0%; Pred. No. 1.1e-28;
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                                                        US-09-961-663-19
                                                                                                                                                                                                                                                                                                ; Sequence 19, Application US/09961663
; General INFORMATION:
APPLICANT: Barnett, Jason
APPLICANT: Beck, James
TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
FILE REFERENCE: PB/5-31382A
CURRENT APPLICATION NUMBER: US/09/961,663
CURRENT FILING DATE: 2001-09-24
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Patent No. US20020115084A1
GENERAL INFORMATION:
                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
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Best Local Similarity
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CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
                  Query Match
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NAME/KEY: misc_feature
LOCATION: (1)..(377)
LOCATION: Tru
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TYPE: DNA
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                                                                        FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Consensus
OTHER INFORMATION: sequence of Mycosphaerella sp. ITS sequences:
OTHER INFORMATION: in SEQ ID NO:14-16.
                                                                                                                                                  LENGTH: 377
TYPE: DNA
ORGANISM: Artificial Sequence
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    DB 9; I
1.1e-28;
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                  Length 377;
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SOFTWARE: Patentin version 3.2

SEQ ID NO 1

LENGTH: 466

TYPE: DNA

ORGANISM: Pestalotiopsis sp. NG12-30

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: GenBank Acc. No. US20040009573A1 AF377301

DATABASE ENTRY DATE: 2002-06-02

RELEVANT RESIDUES: (1)..(466)

US-10-356-320-1
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US-09-961-663-17
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                                   APPLICANT: Barcett, Jason
APPLICANT: Beck, James
APPLICANT: Beck, James
TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
TITLE OF INVENTION: Reaction
FILE REFERENCE: PB/5-31382A
CURRENT APPLICATION NUMBER: US/09/961,663
CURRENT APPLICATION NUMBER: US/09/961,663
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 534
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Matches
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                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/09961663 Patent No. US20020115084A1
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TYPE: DNA
ORGANISM: Mycosphaerella fijiensis
-09-961-663-17
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; ORGANISM: Mycosphaerella musicola
US-09-961-663-18
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              Search completed: October
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US-09-961-663-18
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LENGTH: 540
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Patent No. US20020115084A1
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
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APPLICANT: Beck, James
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100.0%; Pred. No. 1.1e-2
tive 0; Mismatches
              2004, 11:22:42
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Result
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Maximum
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CB900742 tric024xb
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North Carolina State University
Campus Box 7251, Raleigh, NC 27695, U.
Tel: 919-513-0024
Fax: 919-513-0024
Email: ralph_dean@ncsu.edu
Seq primer: LT-F1 primer.
                                                                                                                                                                                                                Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 735)
Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,
Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and
                                                                                                                           Analysis of the protein processing
Trichoderma reesei EST dataset
Unpublished (2003)
Contact: Ralph A. Dean
                                                                                                                                                                                                                                                                                                                                                                                 CF880267 735 bp mRNA linear EST 31-OCT-2003 tric081xc18.b2 T.reesei mycelial culture, Version 6 October 2003 Hypocrea jecorina cDNA clone tric081xc18, mRNA sequence.
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CF800463 6HRm331 6
BM347000 Al 3D11 H
CB012091 Lb5BDD1 m
CB01183 Lb03N02 m
BZ782051 AlSP1C26
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North Carolina State University
Campus Box 7251, Raleigh, NC 27695,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trichoderma reesei EST
Unpublished (2003)
Contact: Ralph A. Dean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D.,
mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Hypocreaceae; 1 (bases 1 to 739)
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Hypocrea jecorina
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primer: LT-F1 primer:
    Location/Qualifiers
29.5%; Silarity 100.0%; Conservative 0;
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                                                                                         /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
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                                                                                                                                                                                                                  /organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
                                                                                                                                                           dev_stage="mycelia"
"Cone_lib="T.reesei mycelial culture, Version 6 October
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/clone_lib="T.reesei mycelial culture,
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|mol_type="mRNA"
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/clone="tric081xc18"
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Score 94; DB;
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Version 6 October 2003
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CB900742 796 bp mRNA linear EST 02-JUL-: tric024xb14 T.reesei mycelial culture, Version 3 april Hypocrea clona clone tric024xb14, mRNA sequence. CB900742 CB900742.1 GI:30115400 EST.
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Trichoderma reesei EST dataset
Unpublished (2003)
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Email: ralph_dean@ncsu.edu
Seq primer: LT-F1_primer.
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Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D
Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordarion
Hypocreomycetidae; Hypocreales; Hypocreae; Hypocreae
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EST.
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                                                                                                                                                                                                             TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGT 96
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                                                                                                                                                                                                                                                                                                                                                                                                                       and Nitrogen sources and concentrations."
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/clone=!tric024xj94"
/dev_stagge="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
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/mol_type="mRNA"
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                                                                           Hypocreomyceracy, 1. (Dases 1 to 808)

1 (Dases 1 to 808)

Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S., Dunn-Coleman, N.S., Goedegebuur, F., Houtek, T. D., England, G.J., Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C., Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M. Transcriptional regulation of biomass-degrading enzymes in th filamentous fungus Trichoderma reesei filamentous fungus Trichoderma reesei T. Biol. Chem. 278 (34), 31988-31997 (2003)
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  Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo A
                                                                                                                                                                                                                                                                                                                                                                                                               CB900860 808 bp mRNA linear ES7
tricO24xj04 T.reesei mycelial culture, Version 3 april
jecorina cDNA clone tricO24xj04, mRNA sequence.
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925 Page Mill Road,
Tel: (650) 846-7635
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Transcriptional regulation of biomass-degrading enzymes in the
                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
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Seq primer: LT-F1 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                              Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
                                                                                                                                                                                                                                                                                                                                                                              CB900860.1 GI:30115518
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J. Biol. Chem. 278 (34), 31988-31997 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (650) 846-7635
(650) 621-7817
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Intl.
Mill Road,
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/strain="QM6a"
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clone="tric024xb14"
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  Palo Alto,
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Pred. No.
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England,G.J.,
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J. Biol. Chem. 278 (
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Foreman, P. K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S., Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J., Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C., Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M. Transcriptional regulation of biomass-degrading enzymes in the
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                                                                                                                                                                                                                                                                      Tel: (650) 846-7635
Fax: (650) 621-7817
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925 Page Mill Road,
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Hypocrea jecorina
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
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tric081xc18 T.reesei mycelial culture, Version 3 april Hypocrea
jecorina cDNA clone tric081xc18, mRNA sequence.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   Contact:
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                                                                                                                                                                                                          il: Pforeman@genencor.com
  primer: LT-F1 primer:
    Location/Qualifiers
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              /clone="tric081xc18"
/dev stage="mycelia"
/dev stage="mycelia"
/clone_lib="T.resei mycelial culture, Version 3
/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycel
culture grown from 24 hrs to 6 days with varying
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and Nitrogen sources
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/mol_type="mRNA"
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/mol_type="mRNA"
/strain="QM6a"
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/clone_lib="T.reesei_mycelial_culture,
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Pred. No. 1.2e-3
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and concentrations."
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Mar 7, 2002 this sequence version replaced Contact: Ebbole DJ Department of Plant Pathology & Microbiology Texas A&M University Peterson Bldg, MSZ132, College Station, TX 77 Tel: 979 845 4831 Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ngns009xJ23f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgns009xJ23 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: d-ebbole@tamu.edu
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person; Best nr hit (April. 22, 2003) gb|AAL79278.1| unknown
resconseromyces cerevisiae] 79 1e-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.

Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: mgns009 row: J
Seg primer: T3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2002)
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/cell_type="mycelium"
/clone lib="Magnaporthe grisea NS Uni-Zap XR Library"
/clone lib="Magnaporthe grisea NS Uni-Zap XR Library"
/note="Wettor: pBluescriptSK-; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Nitrogen starvation library. Cells were inoculated into minimal medium and grown for two days with shaking (150 rpm) at room temperature. Culture was harvested, blended, inoculated into minimal medium as above for 24 h. Cells were harvested, washed with water and inoculated into minimal medium base lacking nitrogen source for 6 h. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredbhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Magnaporthe
/mol_type="mRNA"
/strain="Guyll"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex="Mat1-2 hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="mgns009xJ23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       xref="taxon:148305"
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1.2e-38;
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RESULT 9
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                                                                                                                                                                                                                                                                                 32 AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCAC
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BM347000

Al 3D11 Heterobasidion annosum infection stage cDNA library
Heterobasidion annosum cDNA clone Al 3D11 similar to putative 5.85
ribosomal RNA protein [Arabidopsis thaliana], mRNA sequence.
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Unpublished (2003)
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Agaricales; Schizophyllaceae; Schizophyllum.
1 (bases 1 to 147)
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Southeast MO State University
1 University Plaza, Cape Girardeau,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizophyllum commune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: agathman@semo.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Gathman AC
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Conservative
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3.4e-20;
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Lb08D01 mycelium of Laccaria bicolor grown
bicolor cDNA 5', mRNA sequence.
CB012091
CB012091.1 GI:32334717
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59;
Institut National de la Recherche Agronomique
Centre INRA de Nancy, 54280 Champenoux, France
Tel: +33 383 39 40 80
                                                                                                                                                                          Agaricales; Tricholomataceae; Laccaria.

1 (bases 1 to 374)

Peter,M., Courty,P.-E., Kohler,A., Delaruelle,C., Martin,D.
Tagu,D., Frey-Klett,P., Duplessis,S., Chalot,M., Podila,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 190) Karlsson, M., Olson, A. and Stenlid, J. Expressed sequences from the basidiomycetous tree pathogen Heterobasidion annosum during early infection of Scots pine Fungal Genet. Biol. 39 (1), 51-59 (2003)
                                                                             Analysis of expressed sequence tags basidiomycetes Laccaria bicolor and New Phytol. 159 (1), 117-129 (2003)
                                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Magnus.Karlsson@mykopat.slu.se
Seq primer: 5'TriplEx2 MK Seq.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Forest Mycology & Pathology
Swedish University of Agricultural Sciences
Box 7026, SE-750 07, Uppsala, Sweden
                                                        Equipe de Microbiologie Forestiere
                                                                                                                                                                                                                                                              Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
                                                                                                                                                                                                                                                                                  Laccaria bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +46 18 671806
Fax: +46 18 673599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Magnus Karlsson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Mycelia after 6 h & 72 h of challenge with pine seedling roots" (clone_"lib="Heterobasidion annosum infection stage cDN)
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/clone="A1_3D11"
/tissue_type="Mycelia"
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/strain="TC 32-1 (P)"
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Best Local Similarity
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                                                                                                                                                                                                                                                                          Email: fmartin@nancy.inra.fr
Insert Length: 359 Std Error: 0.00
Seg primer: Fornat 5' AAGCGCGCCATTGTGTTGGTACCC.
                                                                                                                                                                                                                                                                                                                                                                          Equipe de Microbiologie Forestiere
Institut National de la Recherche Agronomique
Centre INRA de Nancy, 54280 Champenoux, France
Tel: +33 383 39 40 80
Fax: +33 383 39 40 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Analysis of expressed sequence tags from the ectomycorrhizal basidiomycetes Laccaria bicolor and Pisolithus microcarpus New Phytol. 159 (1), 117-129 (2003)
Contact: Martin FM
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1 (bases 1 to 359)
Peter,M., Courty,P.-E., Kohler
Tagu,D., Frey-Klett,P., Duples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lb03N02 mycelium of Laccaria bicolor bicolor CDNA 5', mRNA sequence.
CB011883
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Email: fmartin@nancy.inra.fr
Insert Length: 374 Std Error: 0.00
Seg primer: Fornat 5' AAGCGCGCCATTGTGTTGGTACCC.
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Eukaryota; Fungi; Easidiomycota; Hymenomycetes; Homobasidiomycetes;
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                                                                                                          /mol_type="mRNA"
/cultivar="S238N"
/dev_stage="three-weeks-old"
/clone_lib="mycelium of Laccaria bicolor grown for three
                                          /db_xref="taxon:29883"
/dev stage="three-week
                                                                                                                                                                              organism="Laccaria"
                                                                                                                                                                                                                                          ocation/Qualifiers
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'clone_lib="mycelium of Laccaria bicolor grown for three
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/cultivar="S238N"
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Pred. No. 4e-
0; Mismatches
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Duplessis,S., Chalot,M.,
                                                                                                                                                                              bicolor"
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4e-20;
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BZ782051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 789)
Hood,M.E., Antonovics,J. and Koskella,B.
Shared forces of sex chromosome evolution in haploids and diploids
Unpublished (2003)
Contact: Hood ME
Department of Biology
University of Virginia
Gilmer Hall, Charlottesville, VA 22903, USA
Tel: 434 434 5077
Fax: 434 982 5626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: michael.hood@virginia.edu random fragment isolated from Al mating type chromosome; BLASTx similarity to Transcript Antisense to Ribosomal RNA and BLASTn similarity to nuclear ribosomal RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 789.
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country=Italy; common name= anther smut; synonym=Ustilago violacea; Chromosome-specific bands were gel-isolated from electrophoretic karyotypes, triple digested (RsaI, MscI, and DraI), size-fractionated by electrophoresis for fragments between 200 to 1000 bp, cloned, and sequenced."
                                                                                                                                                                             /cell_type="sporidia"
/dev stage="post-meiotic"
/clone_lib="Microbotryum mating type chromosome and
autosome random fragments"
                                                                                                                                                  /note="Field Collected; specific host=Silene latifolia;
                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="I00-15Lamole.1"
/db_xref="taxon:5272"
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                                                                                                                                                                                                                                                                                              clone="A1SP1C26"
                                                                                                                                                                                                                                                                                                                                                                                                            organism="Microbotryum violaceum"
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Pred. No.
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DEFINITION

BZ782081 795 bp DNA linear GSS 14-MAR-3 A1SP2C4 Microbotryum mating type chromosome and autosome random fragments Microbotryum violaceum genomic clone A1SP2C4, genomic

GSS 14-MAR-2003

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RESULT 14
BZ782081
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BZ782064/c
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                                                                                                                                                                   Query Match
Best Local Similarity
Matches 52; Conserv
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Best Local Similarity
Matches 52; Conserv
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                                                                                      695 GATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCA 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Hood ME
Department of Biology
University of Virginia
Gilmer Hall, Charlottesville, VA 22903,
Tel: 434 243 5077
Fax: 434 982 5626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbotryum violaceum
Eukaryota; Fungi; Basidiomycota; Urediniomycetes;
Microbotryomycetidae; Microbotryales; Microbotryaceae;
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AlSP2C19 Microbotryum mating type chromosome and autosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 791.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: michael hood@virginia.edu random fragment isolated from Al mating type chromosome; BLASTx similarity to Transcript Antisense to Ribosomal RNA and BLASTn similarity to nuclear ribosomal RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hood, M.E., Antonovics, J. and Koskella, B. Shared forces of sex chromosome evolution in haploids and diploids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2003)
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                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                  country=Italy; common name= anther smut; symonym=Ustilago violacea; Chromosome-specific bands were gel-isolated from electrophoretic karyotypes, triple digested (RsaI, MscI, and DraI), size-fractionated by electrophoresis for fragments between 200 to 1000 bp, cloned, and sequenced."
                                                                                                                                                                                                                                                                                                                                                                           /dev_Stage="post-meiotic"
/clone lib="Microbotryum mating type chromosome and
autosome random fragments"
/note="Field Collected; specific host=Silene latifolia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic_DNA"
/strain="100-15Lamole.1"
/db_xref="taxon:5272"
/clone="A1Sp2C19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Microbotryum violaceum"
/mol_type="qenomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="sporidia"
                                                                                                                                                                                      16.3%;
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100.0%; Pred. No.
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                                                                                                                                                                                      Score 52;
Pred. No.
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2.4e-16;
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2.4e-16;
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survey sequence

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                    JOURNAL COMMENT
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BZ782314/c
LOCUS
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A2APIC47 Microbotryum mating type chromosome and autosome random
fragments Microbotryum violaceum genomic clone A2APIC47, genomic
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                1 (bases 1 to 840)
Hood,M.E., Antonovics,J. and Koskella,B.
Shared forces of sex chromosome evolution in haploids and Unpublished (2003)
Contact: Hood ME
                                                                                                                                                Microbotryum violaceum
Microbotryum violaceum
Eukaryota; Fungi; Basidiomycota; Urediniomycetes;
Microbotryomycetidae; Microbotryales; Microbotryaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: michael.hood@virginia.edu random fragment isolated from Al mating type chromosome; BLAST: similarity to Transcript Antisense to Ribosomal RNA and BLASTn similarity to nuclear ribosomal RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Hood ME
Department of Biology
University of Virginia
Gilmer Hall, Charlottesville, VA 22903, USA
Tel: 434 243 5077
Fax: 434 982 5626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 795)
Hood, M.E., Antonovics, J. and Koskella, B.
Shared forces of sex chromosome evolution
Unpublished (2003)
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BZ782314.1 GI:28961356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 795.
Location/Qualifiers
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BZ782081.1 GI:28960886
GSS
                                                                                                                                Microbotryum
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Microbotryomycetidae; Microbotryales; Microbotryaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.3%; Score 52; DB 28; ]
.larity 100.0%; Pred. No. 2.4e-16;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="sporidia"
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/dev_stage="post-meiotic"
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/clone_lib="Microbotryum mating type chromosome and
autosome random fragments"
/note="Field Collected; specific host=Silene latifolia;
country=Italy; common name= anther smut; synonym=Ustilago
violacea; Chromosome-specific bands were gel-isolated from
electrophoretic karyotypes, triple digested (RsaI, MscI,
and DraI), size-fractionated by electrophoresis for
fragments between 200 to 1000 bp, cloned, and sequenced."
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/mal_type="genomic DNA"
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ood ME
of Biology
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Search completed: October Job time: 2167.01 secs

October

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                             9 GATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCA
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Gilmer Hall, Charlottesville, VA 22903, USA
Tel: 434 243 5077
Fax: 434 982 5626
Email: michael.hood@virginia.edu
random fragment isolated from autosomes; BLASTx similarity to
Transcript Antisense to Ribosomal RNA and BLASTn similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nuclear ribosomal RNA
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Location/Qualifiers
                                                                                                         Conservative
                                                                                                                                                                                                                              autosome random fragments"
/note="Field Collected; specific host=Silene latifolia;
/country=Italy; common name= anther smut; synonym=Ustilago
violacea; Chromosome-specific bands were gel-isolated from
electrophoretic karyotypes, triple digested (Rsal, Mscl,
and Dral), size-fractionated by electrophoresis for
fragments between 200 to 1000 bp, cloned, and sequenced."
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/db_xref="taxon:5272"
/clone="A2AP1C47"
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Result
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AAV59029

gramin

The present sequence represents an internal transcribed spacer 2 (1782) and adjacent regions. Probes can be derived from the present sequence which are specific. The specification also describes 1782 sequence-derived probes for identifying a species selected from

Claim 1; species.

Page

12; 45pp; English.

New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothr

Sporothrix

WPI; 1999-034737/03.

Morrison

G,

Reiss E,

Aidorevich L, Choi JS;

02-MAY-1997;

97US-0045400P. 98WO-US008926.

01-MAY-1998;

(USSH) US DEPT HEALTH & HUMAN SERVICES

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Aav43269	Aav70847	Abz20765	Aba01153	Aax90108	Aaa72783	Aaz91724	Aaz91723	Abv78715	Abv78718	Aaf76260	Abv78712	Abv78703	Abv78706	Abv78709	Aaz91725	Aax90110	Aat05403	Aat65099	Aas08426	Aat65101	Acc50000	
Sequence	Sequence	Muscodor	Deuteromy	Eutypella	5.8s rRNA	Rosellini	Rosellini	C. sinens	C. sinens	Cordyceps	C. sinens	C. sinens	C. sinens	C. sinens	Rosellini	Phomopsis	Microdoch	T. harzia	Internal	T. harzia	Internal	

ALIGNMENTS

RESULT 1 AAV70851 ID AAV7 XX AC AAV7 XX Gibberella fujikuroi. R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum; Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxil; M. racemosus; M. plumbeus; M. indicus; A. fumigatus; M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus; 12-NOV-1998. WO9850584-A2. Penicillium notatum; Internal transcribed spacer 2 (ITS2) and adjacent regions. 17-OCT-2003 26-FEB-1999 AAV70851; AAV70851 standard; DNA; (revised) (first entry) Sporothrix schenkii; filamentous fungus; ss. 310 BP

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans, Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus, M. indicus, M. circinilloides f. circinelloides, Rhizopus oryzae, R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallesheria boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenkii. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi.
                                                                                                                                                                                                                                                              Gibberellin; 18S rRNA; internal transcribed spacer region; ITS1; 5.8S rRNA; LTB-1027; species differentiation; GA 4; GA 3; GA 7; flowering; fruit cell elongation; apple; pear; grape; fruit;
                                                                                                                                                                                                                                                           5.8S rRNA; LTB-1027; species differentiation; flowering; fruit cell elongation; apple; pear
            misc_feature
                                                    misc_feature
                                                                                              misc_feature
                                                                                                                                      misc_feature
                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                       Gibberella fujikuroi.
                                                                                                                                                                                                                                                                                                                   Fungus genomic DNA spanning 18S,
                                                                                                                                                                                                                                                                                                                                                                                                    AAS16211 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 310 BP; 73 A; 86 C; 80 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                 control; fungus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCAAGCCGTTAAACCCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAAACCCTCGCAACTGGTACGCGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGGGTTTGGTGTTGGGGATCGGCAAGCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGCGCCCGCCAGTATICTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAACTTAA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAAAACCCCTCGCAACTGGTACGCGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                        /note= "ITS2 region"
2244. .2293
/*tag= e
                                                       /note= "5.8S
2079. .2243
                                                                                                                                      /note= "18S rRNA gene"
1775. .1921
                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                   rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 310; DB 2; 1
Pred. No. 5.3e-98;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                   5.8S and 28S rRNA and ITS sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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RESULT 3
ACC50001
ID ACC5
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AC ACC5

ACC50001 standard; DNA; 534 BP

ACC50001;

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Best Local Sim
Matches 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a genomic DNA sequence containing the 18S rRNA gene, internal transcribed spacer regions I and 2 (ITS1, ITS2) and 5.8S rRNA sequences from a mutant strain of Gibberella fukikoroi (LTB-1027) of the invention. This region of DNA is highly variable and can be used for species and strain differentiation. The LTB-1027 mutant produces a mixture of gibberellins which is at least 70 % GA 4 and GA 7. Gibberellins GA 4 and GA 7 promotte flowering and fruit cell elongation, and are used by growers of apples, pears and grapes to produce larger fruits and earlier harveste. The mixture of GA 3, GA 4 and GA 7 achieved using the method of this invention should be particularly useful in the apple industry where GA 4 has been found more effective in russet control and in promoting fruit set. This methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A new method for producing a mixture of gibberellins from fujikuroi results in high titers of GA4 and GA7 useful to flowering and fruit growth in the fruit growing industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2293 BP; 596 A; 527 C; 592 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Col 9-12; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-662197/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallazzo JL, Lee MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-AUG-2000; 2000US-00645073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GALL/) GALLAZZO (LEEM/) LEE M D.
                                                              2212
                                                                                                                                  2152
                                                                                                                                                                                                   2092
                                                                                                                                                                                                                                                                  2032
                                                                                                                                                                                                                                                                                                                                    1972 ÁAATGCGATÁAGTÁATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
                             301
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                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                        CCCGGGTTTGGTGTTGGGGAATCGGCAAGCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTG 180
                                                                                                                                                                                                                                                                                     TIGCGCCCGCCAGIATICIGGCGGGCAIGCCIGIICGAGCGTCATITCAACCCTCAAGCC
                   CTGAACTTAA
                                                                                     GGCCAAGCCGTTAAACCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG
                                                                                                                                                            GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAAACCCTCGCAACTGGTACGCGGCGC
                                                                                                                                                                                                                                                                   TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                GGCCAAGCCGTTAAACCCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG
                                                                                                                                  GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAAACCCTCGCAACTGGTACGCGGCGC
                                                                                                                                                                                                   CCCGGGTTTGGTGTTGGGGATCGGCGAGCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTG
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                             310
                                                                                                                                                                                                                                                                                                                                                                                                                 99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 306.8; DB 4
Pred. No. 1.7e-96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   578 T; 0 U; 0 Other;
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2031

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300

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240

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RESULT 4
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ID AAA6
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AC AAA6
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Best Local :
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             AAA61893
                                     AAA61893 standard; DNA; 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 534 BP; 135 A; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-363229/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-2001; 2001US-00961755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-SEP-2002; 2002WO-US030311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondria; fungal pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JUL-2003
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                                                                                                                                                               GGCCAAGCCGTTAAACCCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG
                                                                                                                                                                                                                  GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAAACCCCTCGCAACTGGTACGCGGCGC
                                                                                                                                                                                                                                                                     CCCGGGTTTGGTGTTGGGGATCGGCAAGCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTG
                                                                                                                          CTGAAC 306
                                                                                                                                                                                                                                                                                                                         TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                                                                                                                                                    GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAAACCCTCGCAACTGGTACGCGGCGC
                                                                                                                                                                                                                                                     CCCGGGTTTGGTGTTGGGGATCGGCGAGCCCTTGCGGCAAAGCCGGCCCCGAAATCTAGTG
                                                                                                                                                                                                                                                                                                       TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                                                                                                                                                                                                                                                                                                       AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 38-39; 44pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   97.7%;
                                     먪
                                                                                                                                                                                                                                                                                                                                                                                                        Score 302.8;
Pred. No. 2.2e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; 130 G; 120 T; 0 U;
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G
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2.2e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 534;
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                                                                                                                                                                                                                                                                                                                      The invention relates to novel steroid compounds derived from the African soil fungus Fusarium sp. WF6381 (ATCC 7448) which act as inhibitors of CHIV integrase. The invention encompasses cultures of Fusarium sp. MF6381. The invention also relates to a composition comprising a compound of the invention in combination with an AIDS antiviral agent, an immunomodulator and an antiinfective agent. The compounds of the invention may be used in the inhibition of HIV integrase and in the prevention and treatment of HIV infection. A wide range of state of HIV infection may be treated: AIDS (acquired immunodeficiency syndrome); ARC (AIDS related complex); both symptomatic and asymptomatic HIV infection; and actual or potential exposure to HIV. The compounds may be used to isolate HIV integrase mutants which are potentially useful as screening tools for antiviral compounds. The compounds may also be used to establish or determine the site at which other antivirals bind to HIV integrase (e.g., by DNA (rDNA) internal transcribed spacer (ITS) region of Fusarium sp. Composition of fusarium sp. wf6381, which may be used to characterise MF6381. (Opdated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 288; Conserv
                                                                                                                                                                                                                                                                                                                    Sequence 502 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Singh SB, Zir
Dombrowski AW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV integrase inhibitor; steroid compound; human immunodeficency virus acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex; symptomatic infection; asymptomatic infection; potential HIV exposure; combination therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 14; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-DEC-1999;
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14-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New steroid compounds are HIV integrase inhibitors used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200036132-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusarium sp; MF6381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribosomal DNA; rDNA ITS region;
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              179
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                                                                      CCCGGGTTTGGTGTTGGGGATCGGCAAGCCCT--TGCGGCAAGCCGGCCCCGAAATCTAG
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TGGCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGAAAACCCTCGCAACTGGTACGCGGC
                                                                                                                                     TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
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                                                 ccceeerrreererreeeeArceeecreceerrcracceeerccceeccceaaarcrae
                                                                                                                 TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0112168P
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                                                                                                                                                                                                                                                                                                                    127 A; 144 C; 118 G; 113 T; 0 U;
                                                                                                                                                                                                                                                              85.7%;
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                                                                                                                                                                                                                                                                 Score 265.8; DB Pred. No. 2e-82;
                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human immunodeficency virus;
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                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                    0 Other;
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                                                                                                                                                                                                                                                                                    502;
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TGGCGGTCTCGCTGCAGCCTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAACGCGGC

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RESULT 5
AAV59009
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   Query Match
Best Local S
Matches 285
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25-MAR-2003
06-JAN-1999
                                                                      This sequence represents an internal transcribed spacer (ITS) sequence of the invention. The primer pairs, based on the ITS sequences, are used for the PCR amplification detection of wheat Microdochium and Fusarium fungal pathogens, especially M. nivale, F. graminearum, F. culmorum, F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different strains of fungi show different symptoms during infection, which may or may not be due to infection. Early identification of the strain causing the infection allows early, and more specific fungicidal treatment. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                          of t
                                                    Sequence 561 BP; 145 A; 152 C; 135 G; 126 T; 0 U;
                                                                                                                                                                                                                                                   Wheat pathogen internal transcribed spacer sequences - used as a basis for primers for the species-specific polymerase chain reaction detection
                                                                                                                                                                                                               Claim 1; Col 29-30; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                  04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                          WPI; 1998-593995/50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibberella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Internal transcribed spacer; ITS; Microdochium; Fusarium; fungal pathogen identification; infection identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Кeу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F. avenaceum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV59009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV59009 standard; DNA; 561
                                                                                                                                                                                                                                         the pathogens.
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                Similarity
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     Conservative
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(revised)
(first en
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/note= "ITS2"
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/note= "ITS1"
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               91.6%;
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Score 249.8; DB 2;
Pred. No. 8.2e-77;
1; Mismatches 23;
   Indels
                          Length
                                                    3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          wheat
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AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60

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                            Query Match
Best Local S
Matches 285
                                                                                                                                                                             Ribosome
of seeds
                                                                                                   The invention relates to a novel base sequence which is part of defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crace. The base sequences can be used for the classification of Cordy sinensis. The sequence represents a C. sinensis rRNA sequence.
                                                                      Sequence
                                                                                                                                                                                                            WPI; 2002-639075/69.
                                                                                                                                                                                                                                (HEAL-)
                                                                                                                                                                                                                                                                                                                                                  Cordyceps sinensis.
                                                                                                                                                                                                                                                                                    12-JAN-2001; 2001JP-00004805.
                                                                                                                                                                                                                                                                                                                              JP2002204696-A.
                                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-2003
                                                                                                                                                                                                                                                               12-JAN-2001; 2001JP-00004805
                                                                                                                                                                                                                                                                                                          23-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                       Cordyceps
                                                                                                                                                                                                                                                                                                                                                                                Ribosome ribonucleic acid; rRNA; Cordyceps crassispora; classification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV78724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABV78724 standard; rRNA; 659
                                                                                                                                                                                                                                                                                                                                                                                                       sinensis
                                                                                                                                                        Page 25; 33pp; Japanese.
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                                                                                                                                                                                                                              HEALTHWAY KK.
KANESHIRO N.
                                        Similarity
                                                                       659
AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
                                                                                                                                                                            RNA gene base sequence of Cordyceps sinensis for classification of Cordyceps sinensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGAACTTAA 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sinensis;
                           80.2%;
nilarity 91.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      rRNA sequence
                                                                      BP; 183
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                         88
                                                                     A; 173
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                           Score 248.6; DB 6;
Pred. No. 2.3e-76;
0; Mismatches 24;
                                                                      C; 160
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                                                                      143
                                                                      T; 0
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                                               Length
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                                                                                                                Cordyceps
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                                                                                                                                                                  The invention relates to a novel base sequence which is part of a fully defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispora. The base sequences can be used for the classification of Cordyceps sinensis. The sequence represents a C. crassispora rRNA sequence of the
                                                                                                                                                                                                                                                  Ribosome :RNA gene base sequence of Cordyceps sinensis for classification of seeds of Cordyceps sinensis.
                                                                                                                                                                                                                                                                                                           (HEAL-)
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                                                                                                                                                                                                                                                                                                                                                                   12-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Cordyceps crassispora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABV78700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABV78700 standard; rRNA; 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             crassispora rRNA sequence
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305
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                                                                                                 h 79.9%;
Similarity 91.6%;
                                                                                                                                                                                                                                                                                                            KANESHIRO
                                                                                                                                                                                                                                                                                                                        HEALTHWAY
                                          AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
                                                                                                                                     647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribonucleic acid;
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                 TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGCCATGCCG-TAAAACCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            sinensis;
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                   2001JP-00004805.
                                                                                                                                    BP; 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
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                                                                                        <u>.</u>
                                                                                                                                    C; 160
                                                                                       Score 247.8; DB 6;
Pred. No. 4.4e-76;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cordyceps crassispora; classification;
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                                                                                                                                    143
                                                                                                                                    T; 0 U;
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                                                                                        Indels
                                                                                                             647;
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364
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ARSSILTY 8
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                                                     The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species-specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from Aspergillus flavus, A. funigatus, A. niger, A. terreus, A. nidulans, P. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus, M. circinalloides f. circinelloides, Rhizopus oryzae, R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallesheria boydii (teleomorph of Scedosporium appiospermum), Pennicillum notatum, or Sporothrix schenkii. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M. circinilloides f. circinelloides; китгория отделення, ка circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum; Penicillium notatum; Sporothrix schenkii; filamentous fungus; вв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus; M. plumbeus; M. indicus; A. fumigatus; M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV70850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 12; 45pp; English
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Best Local
                     This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods and primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present sequence represents an internal transcribed spacer RNA encoding sequence
                                                                                                                             Detecting a fungal pathogen, useful i comprises subjecting the DNA to PCR a primer having sequence identity with of Fusarium spp.
Sequence
                                                                                                     Claim
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This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods ar primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present sequence represents an internal transcribed spacer RNA encoding sequence.

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Best Local S
Matches 258
                                                                                                                                                                                                                                                     Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
                                                                                                                                                                                                          Claim 5;
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of seeds
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The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA gene from the filamentous fungi Trichoderma harzianum strain IMI 3529 A novel liquid formulation based on strains of T. harzianum and T. viride, has the following composition (\(\mu/v\\^2\)): 0.1-6 sorbitol; 0.002-2 K3P03; 0.05-2 KN03; 0.002-1 MgS04.7H30; 0.02-2 (NH4)H2P04; 0.02-2 cop 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron; 0.02-2 molybdenum; 0.02-1 comprising at least one of: T.
                                                                                                                                                                                                                                                                                                                                                                                                                         ITS1-ITS4 region; 5.88 rRNA; filamentous fungi; Trichoderma harzi liquid formulation; T. viride; gene recipient; increase activity; biological control agent; plant disease; biodeterioration; biolixiviation; leaching; ss.
                                                                                                                                      Liquid formulation of Trichoderma harzianum and Trichoderma viride strains - are used as biological control agents against diseases of plants and plant material and as biolixiviation agents.
                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                        07-NOV-1995;
                                                                                                                                                                                                                                                                                                                  06-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                 Hypocrea lixii;
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17-FEB-1998
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ID AAV62
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                                           misc_feature
                                                                                                                                                      misc_feature
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/note= "3'
31. .180
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85.9%;
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Pred. No. 4.7e-57;
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Best Local S
Matches 262
                                                                                                                                                                                                                                                                                                                                                                                                            This represents the consensus DNA sequence of the internal transcribed spacer (ITS) region that was PCR amplified from Fusarium poae isolates, T -427, T-534 and T-756. The invention provides a DNA molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal pathogen, where the DNA molecule consists of an ITS sequence selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium moniliforme, Septoria avenae or Microdochicum nivale. A method for detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F. avenaceum and M. nivale isolates is also provided. The method comprises isolating DNA from a plant leaf infected with at least one of the above pathogens and amplifying parts of the ITS sequence of the pathogen(s) by PCR using specific primers from within these sequences. The pathogen(s) are detected by visualising the amplified part of the ITS sequence
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 546 BP; 150 A; 140 C; 125 G; 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA isolated from fungal RNA, and its internal transcribed spacer sequence - used for detecting fungal pathogens in plant tissue.
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15-OCT-1996;
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                                                                                                                                                                                                                                                                    231
                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                              262;
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                  GGCCAAGCCGTTAAACCCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG
                                                                                                             GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAAACCCTCGCAACTGGTACGCGGCGC
                                                                                                                                                                      CCCGGGTTTGGTGTTTGGGGATCGGCAAGCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTG
                                                                                                                                                                                                          TTGCGCCCGCCAGTATTCTGGCGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                                                                                                                                                                             TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                                                                                                                                                                                                                 AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
                                                                                                                                                                                                                                                                                        AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Col 87-88; 56pp; English.
    CTGAACTTAA 310
                                                                                        GCGGTCACG-TCGAGCTTCCATAGCGTAGTAATTTACACATCGTTACTGGTAATCGTCGC
                                                                                                                                                  C---AGCTTGGTGTTGGG-----ATCTGTGTGCAAACACAGTCCCCAAATTGATTG
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-US004712.
96US-00722187.
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/note= "ITS
490. .546
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/note= "5'
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338. .489
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                                                                                                                                                                                                                                                                                                                           ; Score 187.6; ; Pred. No. 4.9e 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    T; 0 U; 0 Other;
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                                                                                                                                                                    Query Match
                                                                                                                                                                                                                  This sequence represents an internal transcribed spacer (ITS) sequence of the invention. The primer pairs, based on the ITS sequences, are used for the PCR amplification detection of wheat Microdochium and Fusarium fungal pathogens, especially M. nivale, F. graminearum, F. culmorum, F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different strains of fungi show different symptoms during infection, which may or may not be due to infection. Early identification of the strain causing the infection allows early, and more specific fungicidal treatment. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                       Claim 1; Col 25-26; 20pp; English.
                                                                                                                                                                                              Sequence 546
                                                                                                                                                                                                                                                                                                                                                                                            Wheat pathogen internal transcribed spacer sequences - used as for primers for the species-specific polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-593995/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Internal transcribed spacer; ITS; Microdochium; Fusarium; fungal pathogen identification; infection identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F. poae internal transcribed
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06-JAN-1999
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                                                                                                                                                             Local
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                                                             TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
  C---AGCTTGGTGTT
                                                                                              AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
                                                                                                                                               Conservative
                                                                                                                                                                                           BP; 150 A; 140 C; 125 G; 131 T; 0 U; 0 Other;
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/note= "ITS1"
338. .489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "ITS2"
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84.5%;
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NGGG-----ATCTGTGTGCAAACACAGTCCCCAAATTGATTG
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Pred. No. 4.9e-55;
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TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC 120 AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA Matches Query Match Best Local

Similarity

60.2%;

Conservative

1;

Score 186.6; DB 2 Pred. No. 1.1e-54; 1; Mismatches 40

40; 2

Indels 12;

Gaps

271 60 Length 504;

Sequence

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AATO5400
ID AATO5400
XX AATO5
XX AATO5
XX AATO5
XX DT 04-JU
XX Plant
XX CIBP
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                                                                                 A novel method for the detection of plant pathogenic strains of fungi e.g. Septoria nodorum, S.tritici, Pseudocercosporella herpotrichoides, Mycosphaerella fijiensis, M.musicola or Fusarium spp, involves the PCR amplification of sequences found in the internal transcribed region (ITS) of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93 and AAR05357-72. These primers are derived from the ITS sequences of these fungi (AAR05394-T05404 and AAQ94398) and are strain specific. The amplification products of the reactions using these primers can be used with the capture primers AAR05378-93 in colourimetric assays. The primers and ITS DNAs can be used for the detection of specific fungal pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt DNA} encoding intervening transcribed sequence - used for detection plant fungal pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudocercosporella herpotrichoides; Mycosphaerella fijiensis; PCR; Mycosphaerella musicola; amplification; primer; ribosomal RNA gene; internal transcribed region; strain; capture; colourimetric assay; isolate; development; population; random amplified polymorphic DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 54-55; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-383005/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CIBA ) CIBA GEIGY
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                                                             disease development in plant populations
   4 Other;
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Pred. No. 18 the number of results predicted by chance to have а

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS DEFINITION ACCESSION VERSION RESULT 1 AR206401 LOCUS Result No. TITLE 3066.8 30 Score Unknown. Unknown. Unclassified. AR206401 Sequence 7 AR206401 1 (bases 1 to 310) Morrison, C.J., Reiss, E., Aidorevich, L. and Choi, J.Soo. Nucleic acids for detecting Aspergillus species and other filamentous fungi Patent: US 6372430-A 7 16-APR-2002; AR206401.1 Query Match 100.0 10 Length from patent US 6372430. GI:21504992 DB AR206401 BDD03592 AF117922 AF1452903 AF455460 AF455460 AF452163 AF452163 AF452163 AF158304 AF158304 AF158304 AF158307 AF16587 AF1687 AF1687 AF158307 AF1687 AF16887 AF16 ALIGNMENTS 310 ģ DNA linear AF45422 Gibberell AF45460 Gibberell X94176 Pusarium fu X94171 Fusarium pr AF25161 Pythium u AF25161 Pythium u AF25163 Pythium u AF251061 Fusarium AF158304 Fusarium AF158304 Fusarium AF158305 Fusarium AF158307 Fusarium pr U61673 Fusarium pr U61673 Fusarium sp AF165873 Gibberell U34547 Fusarium sp AF158307 Fusarium sp AF158307 Fusarium sp AF158307 Fusarium sp U61692 Fusarium sp U61693 Fusarium sp U61693 Fusarium sp U61694 Fusarium sp U61695 Fusarium sp U61697 Fusarium d U61687 Fusarium n U61688 Fusarium n U61688 Fusarium d U61689 Fusarium sp AF15830 Fusarium sp AF1680 Fusarium sp AR206401 Sequence BD083592 Nucleic a AF117922 Gibberell AF162903 Fusarium Description PAT 20-JUN-2002

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PF 01-MAY-1998 JP 1998548275

PF CTOPOLOGY INDEASON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO PI CHOI

PC C1201/68

CC Strandedness: Single;

CC Topology: Linear;

FH Key Topology: Linear;

FH Key Topology: Linear;

OT TOPOLOGY:
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1 (bases 1 to 310)

Morrison, C.J., Reiss, E., Aidorevich, L. and Choi, J.S.

Nucleic acids for detecting Aspergillus species and other
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Gibberella fujikuroi
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
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/mol_type≈"genomic DNA"
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Gibberella fujikuroi
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Hypocreomycetidae; Hypocreales; Nectriaceae; G
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AF117922 AF117922
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(bases 1 to 310)

Choi,J.S., Westerman,J.M. and Morrison,C.J.

Rapid differentiation of filamentous fungi using species-specific
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                                                                                                                                                                        /product="5.8S ribosomal RNA"
159. .272
                                                                                                                                                                                                                                                                     /organism="Gibberella fujikuroi"
/mol_type="genomic DNA"
/strain="ATCC 38519"
/db_xref="ATCC:38519"
                                                                        product="28S
                                                                                                                                                                                                                                              'db_xref="taxon:5127"
                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                         note="ITS2"
                                                                                                                                              product="internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:5127"
                                                                                                                                                                                                                            . 159
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Pred. No. 1.2e-85
Score 310;
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8
                                                                                                                                                spacer
Length 310;
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; Sordariomycetes; Gibberella; Gibbe

Gibberella

PLN 17-JUN-2000

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VERSION
KEYWORDS
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AF162903
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Best Local
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            82
                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pusarium proliferatum 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosom RNA gene, partial sequence.

AF162903
AF162903.1 GI:5690392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310; Conservative
                                                                                    H
                                                                                                                                                                                                                                                                                                                      Submitted (28-JUN-1999) Biology, Sonor Chong Ro-Gu, Seoul 110-743,
                                                                                                                                                                                                                                                                                                                                                                                               Fusarium proliferatum
Fusarium proliferatum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
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                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                          fujikuroi complex.
1 (bases 1 to 351)
                         TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                         AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA
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                                                           AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
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                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                            Chong Ro-Gu, Seoul 110-
Location/Qualifiers
                                                                                                                                                                                                                                                           /organism="Fusarium proliferatum"
/mol type="genomic DNA"
/strain="6787"
                                                                                                                                                                                  /product="internal transcribed 294...>351
                                                                                                                                                                                                             /product="5.8S ribosomal RNA"
129. .293
                                                                                                                                                                         'product="28S ribosomal RNA"
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                                                                                                          Score 306.8; DB 8;
Pred. No. 1.2e-84;
0; Mismatches 2;
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ORGANISM
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                                 61
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Gibberella fujikuroi isolate wb518 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence.
Ara55422
                                                                                          1 AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Med. Mycol. 41 (2), 149-161 (2003)
2 (bases 1 to 556)
Buzina, W., Braun, H., Freudenschuss, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibberella fujikuroi (anamorph: Fusarium fujikuroi)
Gibberella fujikuroi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-DEC-2001) Laboratory for Mycology and Molecular Biology, ENT-University Hospital, Auenbruggerplatz 26-28, Graz A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fungal biodiversity as found in nasal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stammberger, H.
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TIGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                  TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                       AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
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                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                /product="small subunit ribosomal RNA" 49. .247
                                                                                                                                                                                                                                                                                         /product="5.8S 354. .518
                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/isolate="wb518"
                                                                                                                                                                                                                                    /product="large subunit ribosomal RNA"
                                                                                                                                                                                                                                                                      product="internal transcribed spacer"
                                                                                                                                                                                                                                                                                                                                             'product="internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:5127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Gibberella
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                                                                                                                                                          99.0%;
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                                                                                                                                                            Score 306.8; DB 8; Pred. No. 1.3e-84;
                                                                                                                                             Mismatches
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Submitted (04-DEC-2001) Laboratory for Mycology and Molecular
Biology, ENT-University Hospital, Auenbruggerplatz 26-28, Graz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AP455460 AP455460 AP455460 DNA linear PLN 16-JUN-20 Gibberella fujikuroi isolate wb355 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence. AP455460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gibberella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fungal biodiversity as found in nasal mucus Med. Mycol. 41 (2), 149-161 (2003)

2 (bases 1 to 556)

Buzina, W., Braun, H., Freudenschuss, K., Lack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buzina, W., Braun, H., Freudenschuss, K., Lackner, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tujikuroi
              TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                           AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
                                                                AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
CTGAACTTAA 310
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                                                                                                     99.0%;
ilarity 99.4%;
Conservative
                                                                                                                                                                                                                                                 /product="internal transcribed spacer 1"
248. .353
                                                                                                                                                                                                     'product="internal transcribed spacer
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354. .518
                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:5127"
                                                                                                                                                                                                                                                                                                                                   /organism="Gibberella fujikuroi"
/mol_type="genomic DNA"
/isolate="wb355"
                                                                                                                                                                         product="large subunit
                                                                                                                                                                                                                                                                                          'product="small subunit ribosomal RNA"
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Pred. No. 1.3e-84;
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          /gene="28S rRNA"
501. .>558
/gene="28S rRNA"
                                                                                  /gene="5.8 rRNA"
/product="5.8 ribosomal RNA"
336. .500
                                                                                                                               /gene='
                                                                                                                                                                                                  /product="18S ribosomal RNA"
product="28S ribosomal RNA"
                                                                                                                                                                                                                 gene="18S rRNA"
                                                                                                                                                                                                                                              'gene="18S rRNA"
                                                                                                                                                                                                                                                                    specific_host="rice"
db_xref="taxon:5127"
                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                            "5.8 rRNA"
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FFUJRRNA pene (partial), 5.85 rRNA gene (partial), 5.85 rRNA gene, 285 rRNA gene (partial), 5.85 rRNA gene, 285 rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2).

X94176 X93900

X94176.1 Giill2868

185 ribosomal RNA; 185 rRNA gene; internal transcribed spacer 5.85 ribosomal RNA; 5.85 rRNA gene; internal transcribed spacer internal transcribed spacer 2; ITS1; ITS2.

Gibberella fujikuroi (anamorph: Fusarium fujikuroi)

Gibberella fujikuroi (anamorph: Pusarium fujikuroi)
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Submitted (08-DEC-1995) C. Waalwijk, Research
Protection, PO box 9060, 6700 GW Wageningen, N
On Jun 15, 2001 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waalwijk,C., de Koning,J.R.A., Baayen,R.P. and Gams,W. Discordant groupings of Fusarium spp. from sections Elegans, Liseola and Dlaminia a based on ribosomal ITS1 and ITS2 sequ Mycologia 88, 361-368 (1996)
2 (bases 1 to 558)
Waalwijk,C.
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
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   note="internal transcribed spacer"
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/mol_type="genomic DNA"
/strain="CBS 221.76"
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X94171.1 GI:112873
X94171.1 KINA; 5.8S rRNA gene; internal transcribed internal transcribed spacer 2; ITS1; ITS2.
                                                                                                                                                                                                                                 Submitted (08-DEC-1995) C. Waalwijk, Research Inst. for Plant Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS On Jun 15, 2001 this sequence version replaced gi:1103572. Overlaps with X78260.
                                                                                                                                                                                                                                                                                                                                          Waalwijk,C., de Koning,J.R.A., Baayen,R.P. and Gams,W. Discordant groupings of Fusarium spp. from sections Elegans, Liseola and Dlaminia a based on ribosomal ITS1 and ITS2 sequence Mycologia 88, 361-368 (1996)
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
31. .177
/note="internal transcribed spacer 1,
                                                                                                                                               organism="Fusarium pro/mol_type="genomic DNA"
/strain="CBS 217.76"
                  product="18S ribosomal RNA"
                                                                              gene="18S rRNA"
                                                                                                                                                                                                               Location/Qualifiers
                                               gene="18S rRNA"
                                                                                                                'specific_host="Cattleya"
'db_xref="taxon:42674"
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Pred. No. 1.3e-84;
0; Mismatches 2
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                                                                                                                                                   Direct Submission
Submitted (14-FEB-2003) Environmental Biology,
Guelph, Guelph, ON NIG 2W1, Canada
Location/Qualifiers
                                                                                                                                                                                                                       Fusarium sp. 03001
Fusarium sp. 03001
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 562)
Afunian, M.R. and Hsiang, T.
                                                                                                                                                                                                                                                                                                                                                         AY237110

AY237110

Fusarium sp. 03001 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8 ribosomal RNA gene and in transcribed spacer 2, complete sequence; and 28S ribosomal R gene, partial sequence.

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milarity 99.4%;
Conservative
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/product="5.8 ribosomal RNA"
336. .500
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501. .>558
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178. .335
/product="internal transcribed spacer
187. .345
                                               /product="18S ribosomal RNA"
                                                                           db_xref="taxon:227081"
                                                                                              /mol_type="genomic DNA"
/isolate="03001"
                                                                                                                              organism="Fusarium
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/product="28S
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Pred. No. 1.3e-84;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                        Direct Submission
Direct Submission
Submitted (26-NOV-2001) Plant Pathology, Pennsylvania Submitted (210 Buckhout Laboratory, University Park, Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 569)
Moorman,G.W., Geiser,D.M., Kang,S. and Kim,S.
Pythium species and a population identification
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pythium ultimum var. sporangiiferum Pythium ultimum var. sporangiiferum Eukaryota; stramenopiles; Oomycetes; Pythiales;
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                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 569)
MOOTMan, G.W., Geiser, D.M., Kang, S. and Kim, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pythium ultimum var. sporangiiferum RNA gene, partial sequence. AF452163
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      AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA
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llarity 99.4%;
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                                                                                                                                                          product="18S ribosomal"
                                                                                                                                                                                                                      /organism="Pythium ultimum
/mol_type="genomic DNA"
/variety≈"sporangiiferum"
/isolate="308276R"
                                                                                                                                                                                                  db_xref="taxon:115421"
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511. .>562
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99.4%;
                                                     0;
                                                Score 306.8; DB 8; Pred. No. 1.3e-84; 0; Mismatches 2;
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Pred. No. 1.3e-84;
0; Mismatches 2
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1 (bases 1 to 596)

Kwon,S.-I., van Dohlon,C.D. and Anderson,A.J.

Kwon,S.-I., van analysis of an opportunistic where the state of the state 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (31-JUL-2000) Biology, 84322-5305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Can. J. Bot. 79 (9), 1115-11
2 (bases 1 to 596)
Kwon,S.-I. and Anderson,A.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusarium proliferatum
Fusarium proliferatum
Fusarium proliferatum
Eukaryota, Fungi, Ascomycota, Pezizomycotina,
Hypocreomycetidae, Hypocreales, Nectriaceae, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence; internal transcrib
internal transcribed spacer
RNA, partial sequence.
AF291161
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                                                                                                                                                                                            Similarity
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TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                                 AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA 326
                                                                                                            AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA
                          TTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
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                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                         /note="contains 18S ribosomal
spacer 1, 5.8S ribosomal RNA,
2, 28S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                    /organism="Fusarium proliferatum"
/mol type="genomic DNA"
/strain="NNRL 31071"
/specific_host="Triticum aestivum
/db_xref="taxon:42674"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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99.4%;
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                                                                                                                                                                 Score 306.8; DB 8;
Pred. No. 1.3e-84;
0; Mismatches 2;
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CV.

Super

Dwarf"

spacer

wheat

pathogen,

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; Sordariomycetes; Gibberella; Gibberella

PLN 18-SEP-2001

300 485 240 425 365 120 305

180

Indels Length

<u>,</u>

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RESULT 13
AF158303
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Fusarium
internal
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Gallazzo,J.L. and Lee,M.D.
Production of high titers of gibberellins,
Gibberella fujikuroi strain LTB-1027
Patent: US 6287800-A 1 11-SEP-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR168094
Sequence 1 from
AR168094
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531 bp DNA linear PLN 21-MAR-2000 sp. NRRL26794 18S ribosomal RNA gene, partial sequence; transcribed spacer 1, 5.8S ribosomal RNA gene and internal
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/mol_type="unassigned
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Pred. No. 1.5e-84;
0; Mismatches 2
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RESULT 14 AF158304

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LOCUS DEFINITION

Fusarium sp. NRRL28852 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene and RNA gene, partial sequence.

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Fusarium sp. NRRL 26794
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 531)
O'Donnell,K., Nirenberg,H.I., Aoki,T. and Cigelnik,E.
A multigene phylogeny of the Gibberella fujikuroi species complex:
detectiion of additional phylogenetically distinct species
Mycoscience 41, 61-78 (2000)
2 (bases 1 to 531)
O'Donnell,K.
Direct Submission
Submission
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AF158303
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                                                          GGCCAAGCCGTTAAACCCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG
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170. .328
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/strain="NRRL26794"
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1 (bases 1 to 540)
1 (bases 1 to 540)
O'Donnell,K., Nirenberg,H.I., Aoki,T. and Cigelnik,E.
O'Donnell,K., Nirenberg,H.I., Aoki,T. and Cigelnik,E.
A multigene phylogeny of the Gibberella fujikuroi species complex:
A multigene phylogeny of the Gibberella fujikuroi species complex:
Mycoscience 41, 61-78 (2000)
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Fusarium sp. NRRL 28852
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
AF158302 540 bp DNA linear PLN 21-MAR-20 FUSATIUM Sp. NRRL26427 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and intertranscribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

AF158302
AF158302.1 GI:7106205
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N. University St., Peoria, IL 61604,
Location/Qualifiers
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503. .>540
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|3. .178
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/mol_type="genomic DNA"
/strain="NRRL28852"
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1 (bases 1 to 540)

O'Donnell,K., Nirenberg,H.I., Aoki,T. and Cigelnik,E.

A multigene phylogeny of the Gibberella fujikuroi species complex:
detection of additional phylogenetically distinct species
Mycoscience 41, 61-78 (2000)
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N. University St., Peoria, IL 61604, USA
Location/Qualifiers
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Fusarium sp. NRRL 26427
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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503. .>540
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/mol_type="genomic DNA"
/strain="NRRL26427"
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-905-314A-24
US-09-423-233-6
US-08-652-127C-8
US-08-652-127C-7
US-08-652-127C-5
US-08-652-127C-5
US-08-887-480-82
US-08-887-480-82
US-08-905-314A-12
US-08-915-314A-21
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  RESULT 2
US-09-645-073-1
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γŞ	B 8	D Q	Qу	Db Qy	do Vo	Query Ma Best Loc Matches	RESULT 1 US-09-423-2 Sequence ; Patent NC ; GENERAL I APPLICAN TITLE OF TITLE OF TITLE OF CURRENT CURR		22 22 30 31 33 33 33 33 34 44 44 44 44 44 44 44 44
301 CTG	241 GGC 241 GGC	181 GCG 181 GCG	121 CCO 121 CCO	61 TTGCGC	1 AAA 1 AAA	atch cal Simi 310;	7, 6 NF ON F IN APP SERENCE S		136 1255.2 1255.2 1255.2 1255.2 1255.2 1255.2 1255.2 1255.2 1254.2 1255.2 1254.3 1255.2 1255.
CTGAACTTAA	CAAGCCC CAAGCCC	GICICGO GICICGO	GGGTTTC GGGTTTC		TGCGAT!	larity Conservat	Application 6372430 ORMATION: The Governm NVENTION: Nu NVENTION: Ot. ENCE: 03063- PLICATION NU LING DATE: 2 SEQ ID NOS: PAtentin Ver 10 FUSArium mo FUSArium mo		2 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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	GGCCAAGCCGTTAAACCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG 	GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAAACCCTCGCAACTGGTACGCGGCG 	CCGGGTTTGGTGTTGGGGATCGGCAAGCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTG 	TIGCGCCCGCCAGTATICIGGCGGGCAIGCCTGIICGAGCGTCAITTCAACCCTCAAGC	AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCAC	0%; Score 310; DB 4; 0%; Pred. No. 8.5e-93 0; Mismatches 0	the United States of Acids for Detecting lamentous Fungi US/09/423,233	ALIGNMENTS	1 US-08-742-023-7 3 US-08-968-505-7 3 US-08-986-727-2 4 US-09-423-233-2 3 US-09-037-9908-7 1 US-08-233-608-47 1 US-08-233-608-47 2 US-08-233-608-47 2 US-08-233-28 4 US-09-423-233-28 4 US-09-517-790-5 1 US-08-887-480-85 1 US-08-887-480-85 1 US-08-965-314A-23 1 US-08-968-505-6 1 US-08-933-608-3 1 US-08-233-608-3
	TCGGATCAGGTAGGAATACCCG 300	CCTCGCAACTGGTACGCGGCGC 240	NAGCCGGCCCGAAATCTAGTG 180 NAGCCGGCCCCGAAATCTAGTG 180	GCGTCATTTCAACCCTCAAGCC 120 	TCATCGAATCTTTGAACGCACA 60	Length 310; ; Indels 0; Gaps 0;	f America as Aspergillus Species and		Sequence 7, Appli Sequence 2, Appli Sequence 2, Appli Sequence 7, Appli Sequence 7, Appli Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 28, Appli Sequence 5, Appli Sequence 5, Appli Sequence 65, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

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; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Gibberella fujikuroi
US-09-645-073-1
                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/08905314A Patent No. 5827695
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lee, May
APPLICANT: Galazzo, Jorge
TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7
FILE REFERENCE: L02-01NP
CURRENT APPLICATION NUMBER: US/09/645,073
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,770
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.0
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 308; Conservative
                                                                                                                                                                                                                                           APPLICANT: Beck, James J.

TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                 ZIF: 20779-2257

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COMPUTER: PACENTIN RELEASE #1.0, Version #1.30

CURRENT APPLICATION DATA:
FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                 STATE:
                                  APPLICATION NUMBER:
                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                ADDRESSEE: No. 5827695artis Corporation Patent Department STREET: 3054 Cornwallis Road CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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Pred. No. 2.2e-91;
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; LOCATION: 505..561
; OTHER INFORMATION: /note= "5';
OTHER INFORMATION: xRNA gene"
US-08-905-314A-24
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 80.6%;
Best Local Similarity 91.6%;
                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEPAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 24:
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NAME/KEY: misc_feat
LOCATION: 31..181
OTHER INFORMATION:
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NAME/KEY: misc_feature

* ^^aTION: 182..338

'not
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NAME/KEY: misc feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3'
OTHER INFORMATION: rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 339..504 / OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 182.338
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
531
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                                                                                                                                                                                                                                                                                                                                                                                    285; Conservative
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                       GCTGAACTTAA 310
                                                                                  CGGCCAAGCCGTTAAACCCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCC 299
                                                                                                                                              GGCGGTCTCGCTGCAGCTTCCCATTGCGTAGTAGTAAAACCCCTCGCAACTGGTACGCGGCG
                                                                                                                                                                                          CCCGGGTTTGGTGTTGGGGATCGGCTCTGCCTTMYGGCGGTGCCGCCCCCGAAATACATT
                                                                                                                                                                                                                 CCCGGGTTTGGTGTTGGGGATCGGCAAGCCCTTGCGGC-AAGCCGGCCCCGAAATCTAGT 179
                                                                                                                                                                                                                                                        TTGCGCCCGCTGGTATTCCGGCGGCGATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
                                                                                                                                                                                                                                                                                                                   AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA
                                                                                                                            GGCGGTCTCGCTGCAGCCTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAACGCGGCG
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                                                              CGGCCATGCCG-TAAAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCC 530
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31..181
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541
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                                                                                                                                                                                                                                                                                                                                                                                  ; Score 249.8; 1; Pred. No. 7.8e-
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "5.8S rRNA gene"
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RESULT 4 US-09-423-233-6 ; Sequence 6, Application US/09423233

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RESULT 5
US-08-652-127C-8
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 319
TYPE: DNA ORGANISM: Fusarium solani
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08652127C Patent No. 5792611
ZIP: KIR 6K7

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,1270
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Richar
                                                                                                                                                                                                                                                                                                                        APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        STREET: 850
STREET: 0ttawa
                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                    ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby & MacLean
STREET: 880 Wellington Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294
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277; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATACCCGCTGAACTTAA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTAGTGGCGGTCTCGCTGCAGCTTCCATTGCGTAGTAAAAACCCCTCGCAACTGGTAC
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87.4%;
                                                                                        US/08/652,127C
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Pred. No. 9.1
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                                                                                                                                                                                                                                                                          Suite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Appl Patent No. 57926
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION UNMER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECONMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
                                                                                                               SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: May 23, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                         ALL...
STREET: 86.
TTTY: Ottawa
                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08652127C
                                                                                                                                                                                                                                                                                                                     880 Wellington Street, Suite 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                   George A. Seaby
Seaby & MacLean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.5%;
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RESULT 7
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            ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
RECISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHAN: (613) 232-5815
TELEFRAN: (613) 232-5831
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08652127C Patent No. 5792611 GENERAL INFORMATION:
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Best Local Similarity
Matches 277; Conserv
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: MAY 23, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Richard TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby & MacLean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                        STREET: 880 w
CITY: Ottawa
                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Richard C. Hamelin
VENTION: DETECTION OF PLANT
VENTION: PATHOGEN FUNGI
                                                                                                                                                                                                                                                                                                                                                               Canada
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Pred. No. 9.9e-65,
0; Mismatches 30
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US-08-652-127C-5
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                                                                                                                                MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILLING DATE: May 23, 1996
CILASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEPHONE: (613) 232-5815
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                                                                                 TELEFAX: (613) 232-583 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                          TYPE: nucleic acid
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                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby & MacLean
                IOPOLOGY:
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mes 276; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            880 Wellington Street, Suite 708
                                                                                                  (613) 232-5831
OR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                             Canada
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              linear
                               double
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/722,187
FILING DATE: 15-OCTT-196
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: GGC 1739/P
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAN: 919-541-8587
TELEPAN: 919-541-8689
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 Dase pairs
TYPE: NUCLEIC acid
CTTANANTENNESS: single
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US-08-887-480-96
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GENERAL INFORMATION:
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Best Local Similarity 85.0
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Beck, James J
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
MOLECULE TYPE:
ORIGINAL SOURCE:
STRAIN: Fusar
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                         STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10591
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Fusarium poae
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                                     DNA (genomic)
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85.0%; Pred. No. 1.1e-55;
tive 0; Mismatches 37;
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Sequence 22, Application US/08905314A Patent No. 5827695
GENERAL INFORMATION:

APPLICANT:

Beck, James J

OF WHEAT FUNGAL POLYMERASE CHAIL

PATHOGENS N REACTION

Patent Department

TITLE OF INVENTION: DETECTION OF WHEAT FUN
TITLE OF INVENTION: USING THE POLYMERASE C
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827695artis Corporation
STREET: 3054 Cornwallis Road

CITY: Research Triangle Park STATE: NC

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; LOCATION: Misc_feat; LOCATION: 490..546; OTHER INFORMATION: /n.; OTHER INFORMATION: rR. US-08-887-480-96
RESULT 10
US-08-905-314A-22
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Best Local Similarity
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INDIVIDUAL ISOLATE:
IMMEDIATE SOURCE:
CLONE: pCRFpoaeT427(
CLONE: pCRFpoaeT756(
FEATURE:
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NAME/KEY: misc_feature
LOCATION: 181.337
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                                                                                            CTGAACTTAA 310
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                                                                                                                                                                                                                                                  C---AGCTTGGTGTTGGG------ATCTGTGTGCAAACACAGTCCCCAAATTGATTG 398
                                                             CTGAACTTAA 526
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rRNA gene"
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Pred. No. 2.5e-52;
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Best Local Similarity
Matches 262; Conserv
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
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INDIVIDUAL:ISOLATE: T-427, T-534, and T-756 (consensus
INDIVIDUAL ISOLATE: sequence)
IMMEDIATE SQURCE:
CLONE: pCRFpoaeT427(1-2), pCRFpoaeT534(2-2), and
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ORIGINAL SOURCE:
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LOCATION: 490..546
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
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LOCATION:
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LOCATION:
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181 GCGGTCTCCGCTGCAGTTCCATTGCGTAGTAGTAAAACCCTCGCAACTGGTACGCGGCGC 240
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                                                      C---AGCTTGGTGTTGGG-----ATCTGTGTGCAAACACAGTCCCCAAATTGATTG
                                                                                  CCCGGGTTTGGTGTTGGGGATCGGCAAGCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTG 180
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pCRFpoaeT756(3-1)
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338..489
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rRNA gene"
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Pred. No. 2.5e-52;
0; Mismatches 34
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TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,24
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ORIGINAL SOURCE:
ORGANISM: Fusarium culmoru
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REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
                                                                                                           FEATURE:
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TITLE OF INVENTION: Detection of Fungal Pathogens Using
TITLE OF INVENTION: Polymerase Chain Reaction
NAME/KEY:
LOCATION:
                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: 1..12
OTHER INFORMATION: /note= "3'
OTHER INFORMATION: rRNA gene"
                                                                  NAME/KEY: misc_feature
LOCATION: 162.318
                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                 ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
INDIVIDUAL ISOLATE: (consensus sequence)
                                                                                                                       OTHER INFORMATION: /note=
                                                                                                                                            LOCATION:
                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 504 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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RESULT 12
US-08-905-314A-19
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TELEPAX: (91y)
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5827695
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILLING DATE:
CLASSIFICATION: 435
                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEPAX: (919) 541-8689
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Beck, James J.

TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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LOCATION: 473..50;
OTHER INFORMATION: /note= "5'
OTHER INFORMATION: rRNA gene"
                                                                                                                                                                                                                                                                                                                          ZIP: 20779-2257
                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     CITY: Research Triangle Park
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o. 5827695
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Pred. No. 5.2e-52;
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RESULT 13
US-08-722-187-82
; Sequence 82, Application US/08722187
; Patent No. 595374
; GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
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Best Local S
Matches 252
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NAME/KEY:
LOCATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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LOCATION: 473..504
OTHER INFORMATION: /note= "5'
OTHER INFORMATION: rRNA gene"
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les 252; Conserv
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LOCATION: 162..318
OTHER INFORMATION:
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rRNA gene"
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Pred. No. 5.2e-52;
1; Mismatches 40
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RESULT 14
PCT-US95-04712-82
; Sequence 82, Application PC/TUS9504712
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
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Best Local Sim
Matches 252;
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ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-866
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 1..504
OTHER INFORMATION: /note
OTHER INFORMATION: inter
OTHER INFORMATION: (fcul
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HYPOTHETICAL:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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nilarity 82.6%;
Conservative
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internal transcribed.
(fculm.con)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 186.6; DB 2;
Pred. No. 5.2e-52;
1; Mismatches 40;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/233,6
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEPHONE: 919-541-8666
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: 8ingle
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: DNA (genomic)
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Best Local (
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NAME/KEY: misc feature
LOCATION: 1.504
OTHER INFORMATION: /note
OTHER INFORMATION: inter
OTHER INFORMATION: (fcul
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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CITY: Hawthorne
STATE: NY
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                                                     GGCCAAGCCGTTAAACCCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG
                                                                                                                          GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAAAAACCCTCGCAACTGGTACGCGGCGC
CTGAA 305
                                                                                                                                                                                                                                                                                                                                       AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA
                               GGCYACGCCGTTAAA-CCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG
                                                                                                  GCGGTCACGTCGRAGCTTCCATAGCGTAGTAATTTACATATCGTTACTGGTAATCGTCGC
                                                                                                                                                                          C---AGCTTGGTGTTGGG----
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internal transcribed
(fculm.con)"
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; Pred. No. 5.2e
1; Mismatches
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hes 40;
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US-08-986-727-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: EKST.com, Richard C.
REGISTRATION UNMBER: 37,027
REFERENCE/DOCKET NUMBER: 009773-012
REFERENCE/DOCKET NUMBER: 009773-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 611 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,727
FILING DATE: 08-DEC-1997
CLASSIFICATION: 435
CMCCANTON APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 59.7
Best Local Similarity 83.1
Matches 260; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08986727 Patent No. 6080543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: ENGEL, Stacia R.
APPLICANT: DESCENZO, Richard A.
APPLICANT: IRELAN, NANCY A.
TITLE OF INVENTION: DETECTION OF FUNGAL PATHOGENS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. STREET: P.O. Box 1404
                                                                          518
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                       CCGCTGAACTTAA 310
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CCGCTGAACTTAA 590
                                                                          GGTGCCCTGCCGTTAAACCCCCAACTTCTGAAAGTTTGACCTCGGATCAGGTAGGAATAC
                                                                                                                                                 GCGAGCTCGC--CAGGACCCCGAGCGCAGTAGTTAAACCCTCGCTCCGGGAGGCCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.7%; Score 185; DB 3; Length 611; 83.1%; Pred. No. 1.9e-51; ative 0; Mismatches 45; Indels
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Search completed: October 1, 2004, 08:05:40 Job time: 103.159 secs

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                      Published Applications NA:*

1: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*

4: /cgn2 6/ptodata/1/pubpna/US06 PUBCOMB.seq:*

5: /cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

7: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

10: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

11: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

12: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*

13: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*

14: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*

15: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*

16: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*

16: /cgn2 6/ptodata/1/pubpna/US108 PUBCOMB.seq:*

16: /cgn2 6/ptodata/1/pubpna/US108 PUBCOMB.seq:*

16: /cgn2 6/ptodata/1/pubpna/US108 PUBCOMB.seq:*

16: /cgn2 6/ptodata/1/pubpna/US108 PUBCOMB.seq:*
                                                         Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

14	13	12	11	10	9	8	7	6	5	4	ω	N	1	Result No.
124.2	124.2	124.6	125	131.4	136	136.2	136.2	179.2	194.4	194.4	240.2	302.8	310	Score
40.1	40.1	40.2	40.3	42.4	43.9	43.9	43.9	57.8	62.7	62.7	77.5	97.7	100.0	Query Match 1
650	650	641	309	364	365	652	652	521	522	522	319	534	310	Length DB
17	15	9	15	15	15	17	15	10	10	10	15	10	15	: H
US-10-623-432-4	US-10-121-740-4	US-09-766-173C-4	US-10-046-955-28	US-10-046-955-2	US-10-046-955-3	US-10-623-432-2	US-10-121-740-2	US-09-961-755A-6	US-09-961-755A-8	US-09-961-755A-5	US-10-046-955-6	US-09-961-755A-7	US-10-046-955-7	ID
Sequence 4, Appli	Sequence 4, Appli	#	Sequence 28, Appl	Sequence 2, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 5, Appli	Sequence 6, Appli	Sequence 7, Appli	Sequence 7, Appli	Description

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AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA

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45	C 44	43	42	41	40	39	38	37	36	c 35	34	33	c 32		30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15
54.4	٠	55.8	٠	59.4	59.4	59.4	60.8	77	82.4	90.4	90.4	90.4	90.4	90.4	99.6	100.2	107.2	107.2	107.8	108.4	108.8	110	110.4	110.4	110.4	110.4	111.6	111.6	120.2	123.2
17.5	17.6	18.0	18.8	19.2	19.2	19.2	19.6	24.8	26.6	29.2	29.2	29.2	29.2	29.2	32.1	32.3	34.6	34.6	34.8	35.0	35.1	35.5	35.6	35.6	35.6	35.6	36.0	36.0	38.8	39.7
1916	876	1235	102	330	328	327	330	117	377	3480	754	754	228	219	156	355	540	346	346	534	336	466	377	377	377	377	344	343	618	365
13	9	17	15	15	15	25	15	15	17	15	17	17	15	15	15	15	9	15	15	9	15	16	9	9	9	9	15	15	9	15
US-10-424-599-82575	US-09-897-231-6	US-10-437-963-59964	US-10-083-357-360	US-10-046-955-12	US-10-046-955-9	US-10-046-955-10	US-10-046-955-8	US-10-083-357-372	US-10-358-929A-3	US-10-297-621-2	US-10-358-929A-5	US-10-358-929A-4	US-10-083-357-71	US-10-083-357-72	US-10-254-657-1	US-10-046-955-4	US-09-961-663-18	US-10-046-955-24	US-10-046-955-25	US-09-961-663-17	US-10-046-955-29	US-10-356-320-1	US-09-961-663-19	US-09-961-663-16	US-09-961-663-15	US-09-961-663-14	US-10-046-955-26	US-10-046-955-27	US-09-766-173C-5	US-10-046-955-5
Seguence 82575. A	Sequence 6, Appli	59964	360,	12,	Sequence 9, Appli			Sequence 372, App		2	<u>ა</u>		71,	72,	1,	e 4,	18, /	24,	25,		29,	e 1,	19,	16,	15,	14, A	Sequence 26, Appl	27	Sequence 5, Appli	Sequence 5, Appli

ALIGNMENTS

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US-10-046-955-7
; Sequence 7, Application US/10046955
; Publication No. US20030129500A1
GENERAL INFORMATION;
GENERAL INFORMATION;
GENERAL INFORMATION:
CONTROL and Prevention
APPLICANT: Choristine J.
APPLICANT: Merison, Christine J.
APPLICANT: Addoravich, Liliana
APPLICANT: Addoravich, Liliana
APPLICANT: Addoravich, Liliana
APPLICANT: Addoravich, Liliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT PILNG DATE: 1002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILLING DATE: 2000-06-627
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILLING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILLING DATE: 1998-05-02
NUMBER: OF SEQ ID NOS: 61
SEQ ID NO 7
LENGTH: 310
TYPE: DNA
ORGANISM: Fusarium moniliforme
US-10-046-955-7
Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e-103;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
APPLICANT: Beck, Jim
APPLICANT: Bernett, Jason
APPLICANT: Bernett, Jason
APPLICANT: Bernett, Jason
FITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 60055
CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
TYPE: DNA
ORGANISM: Fusarium proliferatum
US-09-961-755A-7
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US-09-961-755A-7
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Best Local Similarity 99.3
Conservative
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                            CTGAAC 306
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CTGAAC 534
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Pred. No. 3.5e-100;
0; Mismatches 2;
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RESULT 3

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APPLICANT: Aldorevich, Liliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Spec
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR APPLICATION NUMBER: US 09/423,230
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR PILING DATE: 1997-05-02
NUMBER OF ESO ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
CRGANISM: FUSSATium solani
FUSANISM: FUSSATium solani
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US-09-961-755A-5
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Publication No. US20030129600A1
GENERRAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dist APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
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Best Local S
Matches 277
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APPLICANT: Beck, Jim
APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Fusarium Species infecting
TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 60055
CURRENT APPLICATION UNDBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
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87.4%;
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                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09961755A
Publication No. US20030113722A1
GENERAL INFORMATION:
APPLICANT: Beck, Jim
APPLICANT: Beck, Jim
APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 60055
                                                                                                                                                                                                                 SEQ ID NO 8
LENGTH: 522
TYPE: DNA
ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
S-09-961-755A-8
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LENGTH: 522
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Best Local (
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CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
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Pred. No. 2.1e-60;
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US-09-961-755A-6
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RESULT 7
US-10-121-740-2
; Sequence 2, Application US/10121740
; Publication No. US20030186425A1
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Strobel, Gary
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND TITLE OF INVENTION: USE
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019-40
; CURRENT APPLICATION NUMBER: US/10/121,740
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Fusarium Species infecting
TITLE OF INVENTION: Delymerase Chain Reaction
FILE REFERENCE: 60055
CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 521
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Best Local Similarity
Matches 255; Conserv
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TYPE: DNA
ORGANISM: Gibberella
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Pred. No. 7.9e-55;
0; Mismatches 38;
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; PRIOR FILING DATE: 2002-03-11; PRIOR APPLICATION NUMBER: 60/363,072; PRIOR APPLICATION NUMBER: 2001-04-16; NUMBER OF SEQ ID NOS: 4; SOPTWARE: FastSEQ for Windows Version 4.; SEQ ID NO 2; LENGTH: 652; LENGTH: 652; ORGANIGM: Muscodor albus US-10-121-740-2
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                                                                                                                                        ; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 2
; LENGTH: 652
; TYPE: DNA
; ORGANIAM: Muscodor albus
US-10-623-432-2
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US-10-623-432-2
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CURRENT APPLICATION NUMBER: US/10/623,432
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: US/10/121,740
PRIOR FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/283,902
PRIOR APPLICATION NUMBER: 60/283,902
PRIOR PRICING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: 60/363,072
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
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                                                            Query Match
Best Local Similarity
Matches 223; Conserv
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Best Local Similarity
Matches 223; Conserv
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Publication No. US20040141955A1
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Strobel, Gary
APPLICANT: Manker, Denise
TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS
TITLE OF INVENTION: USE
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                       GCTGAACTTAA 310
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 AAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA 388
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                                                                       Conservative
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71.7%;
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                                                                    Score 136.2; DB 17;
Pred. No. 5.3e-39;
0; Mismatches 78;
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                                                                     Indels
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TITLE OF INVENTION: Other filamentous Fungi
FILE OF INVENTION: Other filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US/9/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: US/9/423,233
PRIOR FILING DATE: 1090-06-27
PRIOR APPLICATION NUMBER: US/9/423,233
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US/0/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
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US-10-046-955-3
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Publication No. US20030129600A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dise APPLICANT: Control and Prevention
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 218; Conserv
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APPLICANT:
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                                                                                            CCCGGGTTTGGTGTTGGGGATCGGCAAGCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTG
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                                  GCGGTCTCGCTGCAGCTTCCATTGCGTA-----GTAGTAAAACCCTCGCAACTGGTACG
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 GCGGCACCGCGTCCGATCCTCGAGCGTATGGGGCTTTGTCACCTGCTCTGTAGGCCCCGGC
                                                                                                                                             TTGCGCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAG--
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Choi, Jong Soo
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Pred. No. 4.7e-39;
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US-10-046-955-28
; Sequence 28, Application US/10046955
; Publication No. US20030129600A1
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; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-046-955-2
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US-10-046-955-2
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Publication No. US20030129600A1
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PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Aidorévich, Liliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
FULL REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
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PRIOR FILING DATE: 1998-05-01
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                                                                                                           CCGCTGAACTTAA
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                                                                                                                                                                                                                                                     GCGGCACCGCGTCCGGGTCCTCGAGCGTATGGGGCTTGTCACCTGCTCTGTAGGCCCGGCC
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68.1%;
                                                                                                           363
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Pred. No. 2.3e-37;
0; Mismatches 96
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GENERAL INFORMATION:

APPLICANT: Carroll, George C.

APPLICANT: Carroll, George C.

TITLE OF INVENTION: Materials and Methods For Detection of TITLE OF INVENTION: Pathogenic Guignardia Citricarpa FILE REFERENCE: Oregon 99-09

CURRENT APPLICATION NUMBER: US/09/766,173C

CURRENT APPLICATION NUMBER: PCT/US01/01735

PRIOR APPLICATION NUMBER: PCT/US01/01735

PRIOR APPLICATION NUMBER: PCT/US01/01735

PRIOR APPLICATION NUMBER: BC0/177,013

PRIOR FILING DATE: 2000-01-19

NUMBER: OF SEQ ID NOS: 13

PRIOR FILING DATE: 2000-01-19
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TITILE OF INVENTION: Nucleic Acids for Detecting Asg
TITILE OF INVENTION: Ocher Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR APPLICATION NUMBER: DCT/US98/08926
PRIOR FILING DATE: 1900-06-27
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-766-173C-4
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LENGTH: 309
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Local Similarity 69.0%;
les 216; Conservation
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FastSEQ for Windows Version
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Pred. No. 4.7e-35;
0; Mismatches 90;
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Strobel, Gary

APPLICANT: Manker, Denise

TITLE OF INVENTION: USE

FILE REFERENCE: AQ 2019.40

CURRENT APPLICATION NUMBER: US/10/121,740

CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: 60/283,902

PRIOR APPLICATION NUMBER: 60/283,902

PRIOR APPLICATION NUMBER: 60/363,072

PRIOR APPLICATION NUMBER: 60/363,072

PRIOR FILING DATE: 2001-04-16

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 650
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                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Muscodor roseus
US-10-121-740-4
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US-10-121-740-4
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; LENGTH: 641
; TYPE: DNA
; ORGANISM: Guignardia Citricarpa
US-09-766-173C-4
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Best Local Similarity
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Best Local Similarity 64.6%;
Matches 201; Conservative
                                                                                                                                                                                                 Matches 222;
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                                                                          61 TIGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
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CCCGGGTTTGGTGTTGGGGATCGGCAAGCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTG 180
                                                     TTGCGCCCATTAGCATTCTAGTGGGCATGCCTGTTCGAGCGTCATTT-ACCACTTAAGCC
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                                                                                                                                                                                               Score 124.2; DB 15; Length Pred. No. 1.3e-34; O; Mismatches 78; Indels
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Pred. No. 9.4e-35;
0; Mismatches 109
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; ORGANISM: Muscodor roseus
US-10-623-432-4
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US-10-623-432-4
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4
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APPLICANT: Strobel,
APPLICANT: Manker,
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Best Local Similarity 71.4%;
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TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI
TITLE OF INVENTION: US
FILE REFERENCE: AQ 2019.40
CURRENT APPLICATION NUMBER: US/10/623,432
CURRENT FILING DATE: 2003-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/83,902
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: 60/363,072
PRIOR FILING DATE: 2001-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-07-17 PRIOR APPLICATION NUMBER: US/10/121,740
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619
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                                GCTGAACTTAA 310
                                                                                                                                       GCGGAGTTGGTTC----TCACTCTAGGCGTAGTAAATCTATCTCGCCTCTGTAGTGGTTC
                                                                                                                                                                      GCGGTCTCGCTGCAGCTTCCATTGCGTAGTAGTAAAACCCTCGCAACT-GGTACGCGGCG
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                                                                  CGGCCCCTGCCGTAAAACCCCCCTATATCAAAGGTTGACCTCGGATCAGGTAGGAATACCC
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    TCACTCTAGGCGTAGTAAATCTATCTCGCCTCTGTAGTGGTTC

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Pred. No. 1.3e-34;
0; Mismatches 78;
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RESULT 15 US-10-046-955-5 ; Sequence 5, Ap;

Application US/10046955

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APPLICANT: Aidorevich, Liliana
APPLICANT: Choi, Jong Soo
ITITE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
ITITE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR APPLICATION NUMBER: DCT/US98/08926
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR PILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
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Search completed: October 1, Job time: 1263.46 secs
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; TYPE: DNA
; ORGANIZM: Aspergillus nidulans
US-10-046-955-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 39.7%; Score 123.2; DB 15; Length 365; Best Local Similarity 66.2%; Pred. No. 2.3e-34; Matches 208; Conservative 0; Mismatches 102; Indels 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention APPLICANT: Morrison, Christine J. APPLICANT: Reiss, Errol
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                                                                                                                                                                                                                           237 GCGCGGCCAAGCCGTTAAACCCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATA 296
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Listing first 45 summaries
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Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 2769
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph dean@ncsu.edu
Seq primer: LT-F1 primer.
                                                                                                                                                                                                                                                                                                            739 bp mRNA linear EST 31-OCT-2003 tric024xb14.bl T.reesei mycelial culture, Version 6 October 2003 Hypocrea jecorina cDNA clone tric024xb14, mRNA sequence.
CF870552
                                                                                                    Analysis of the protein processing and Trichoderma reesei EST dataset Unpublished (2003)
Contact: Ralph A. Dean
                                                                                                                                                                         Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (Dases 1 to 739)
Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,
Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and
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Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 755)
Diener S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,
Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and
                                                                                                                                                                                                                                                                                                                                                    cra/ubbb mRNA tric024xj04.bl T.reesei mycelial culture, Hypocrea jecorina cDNA clone tric024xj04, CF870665
                                                          Fax: 919-513-0024
              Email: ralph_dean@ncsu.edu
Seq_primer: LT-F1 primer.
Location/Qualifiers
                                                                                                                                                                   Trichoderma reesei
                                                                                                                                      Unpublished (2003)
Contact: Ralph A. Dean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
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/clone_lib="T.reesei mycelial culture,
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/clone="tric024xb14"
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|mol_type="mRNA"
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Hypocrea jecorina (anamorph: Trichoderma reesei)

SM Hypocrea jecorina

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Eukaryota; Fungi; Ascomycota; Pezizomycetae; Hypocrea.

25 1 (bases 1 to 796)

1 (bases 1 to 796)

26 Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,

Bunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,

Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,

Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.

Transcriptional regulation of biomass-degrading enzymes in th
filamentous fungus Trichoderma reesei

J. Biol. Chem. 278 (34), 31988-31997 (2003)
                                         Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto,
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
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                                                                                       Palo Alto,
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culture, Version 3 april Hypocrea 14, mRNA sequence.

Sordariomycetes;

enzymes in the

mRNA

linear

EST 02-JUL-2003

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94304, USA

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1 AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA
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                              CGGCCAAGCCGTTAA----ACCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATA
                                                                                                         GCGGTCTCGCCGCAGCCTCTCCTGCGCAGTAGTTTGCACACTCGCACCGGGAGCGCGGCG
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CGGCCACAGCCGTAAAACACCCCCAAACTCTGAAATGTTGACCTCGGATCAGGTAGGAATA
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/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
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/mol type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
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Pred. No. 1.1e-43;
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                                                                                                                                                                                                                    Hypocrea jecorina (anamorph: Trichoderma reesei)

SM Hypocrea jecorina

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Hypocreacea; Hypocrea.

1 (bases 1 to 808)

E foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,

Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,

Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,

Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.

Transcriptional regulation of biomass-degrading enzymes in the

filamentous fungus Trichoderma reesei

J. Biol. Chem. 278 (34), 31988-31997 (2003)
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                                                                                                                                    Genencor Intl.
925 Page Mill Road,
                                                                                                                                                                   12788920
Contact: Pamela K. Foreman
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                                                                 il: Pforeman@genencor.com
primer: LT-F1 primer.
                                                                                                    (650) 846-7635
(650) 621-7817
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/dev stage="mycella"
/dev stage="mycella"
/clone_lib="T.reesei mycelial culture, Version 3 april"
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
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/organism="Hypocrea jecorina"
                                                 Location/Qualifiers
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/mol_type="mRNA"
/strain="QM6a"
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Pred. No. 1.1e-43;
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VERSION
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                     Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
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                                                                                Fax: 919-513-0024
Email: ralph dean@ncsu.edu
Seq primer: LT-F1 primer.
Location/Qualifiers
                                                                                                                                                                                   Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27
                                                                                                                                                                                                                                                                 Trichoderma reesei
Unpublished (2003)
                                                                                                                                                                                                                                                                                                         Analysis of the protein processing
                                                                                                                                                                                                                                                                                                                              Dean, R.A.
                                                                                                                                                                                                                                                                                                                                               Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfel Mitchell, T.K., van Solingen, P., Teunissen, P.J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF880267.1 GI:38134949
                                                                                                                                                                                                                                              Contact: Ralph A. Dean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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/organism="Hypocrea
/mol_type="mRNA"
/strain="QM6a"
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/clome_lib="T.reesei mycelial culture, Version 3 april"
/clome_rivector: prEPPY; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
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/clone="tric024xj04"
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/strain="QM6a"
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Pred. No. 1.1e-43;
                                                                                                                                                                                                                                                                                        dataset
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Version 6 October 2003
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RESULT 6
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                                                                                                                                                                                                                                              Genencor Intl.
925 Page Mill Road, I
Tel: (650) 846-7635
Fax: (650) 621-7817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
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                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 840)

Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S., Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J. Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C., Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.

Transcriptional regulation of biomass-degrading enzymes in tilamentous fungus Trichoderma reesei

J. Biol. Chem. 278 (34), 31988-31997 (2003)
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12788920
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                                                                                                                                                                                                                                                                                                                          Contact: Pamela K. Foreman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
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                                                                                                                                                                             il: Pforeman@genencor.com
primer: LT-F1 primer:
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 3 apr
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon
                                                                 /db_xref="taxon:51453"
/clone="tric081xc18"
                                                                                                                      organism="Hypocrea jecorina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
^^^"
                                                                                                        strain="QM6a"
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Pred. No. 4.1e-30;
Pred. No. 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
BQ751285
BQ751285.1 GI:21906690
EST.
Colletotrichum trifolii
Colletotrichum trifolii
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                                                                                                                                                                                                                                                     Email: debbys@puccini.crl.umn.
TIGR sequence name: MTSAD17TV
                                                                                                                                                                                                                                                                                                                           Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                            Other_ESTs: EST631847
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                       Cheung, F. and Fraser, C.M.
ESTs from mycelia of Colletotrichum
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                                                                                                                                                                                                                                            www.medicago.org
                                                                                                                                                                                                                                                                                      Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                                                                                                                    Samac, D.A., Dickman, M.,
                                                                                                                                                                                                                                                                                                                  195 Borlaug Hall, 1991 Upper Buford
                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitosporic Phyllachoraceae; Colletotrichum.
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                                                              /dev_stage="Young, actively of inoculation) grown in liquid containing 2*glucose)."
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Location/Qualifiers
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/note="Vector: pBluescript SK+; Site_l: EcoRI; Site_2:
EcoRI; isolate: 2sp2 ; cDNA was prepared from polyA+
                                                                                                          /clone="pDSCT4-17"
/tissue_type="mycelia"
                                                                                                                                       db_xref="taxon:5466"
                                                                                                                                                      /mol_type="mRNA"
/strain="race 1"
                                                                                                                                                                                organism="Colletotrichum"
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                                                lab_host="DH5alpha"
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78.0%;
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Pred. No. 4.4e-30
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pDSCT4-17, mRNA
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                                                                                                                                                                                                                                                                             495 Borlaug Hall, 1991 Upper Buford Circle,
Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                            Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 725)
Samac, D.A., Dickman, M., Town, C.D., V
Cheung, F. and Fraser, C.M.
ESTs from mycelia of Colletotrichum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.
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EST632564 DSCT Colletotrichum
                                                                                                                                                                                                                                Email: debbys@puccini.crl.umn.
TIGR sequence name: MTSAI22TV
                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
Other_ESTs: EST632563
                                                                                                                                                                                                         www.medicago.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colletotrichum trifolii
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/db_xref="taxon:5466"
/clone="pDSCT9-22"
/tissue_type="mycelia"
                                                                          /mol_type="mRNA"
/strain="race 1"
                                                                                                                  organism="Colletotrichum"
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Pred. No. 2.4
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m trifolii cDNA clone
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pDSCT9-22, mRNA
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ACCESSION VERSION

BQ752001 LOCUS

DEFINITION

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KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS

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RESULT 9 BQ751015

DEFINITION

닭 á 밁 Ś 밁 á 밁 ঠ 밁 8

Matches

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TITLE JOURNAL

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Query Match
Best Local (
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BQ751015
BQ751015.1
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EST631578
                                                                                                                                                                    Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Ut Cheung,F. and Fraser,C.M.
ESTS from mycelia of Colletotrichum trifolii race Unpublished (2002)
Other_ESTs: EST631577
Contact: Deborah A. Samac Department of Plant Pathology University of Minnesota 495 Borlaug Hall, 1991 Upper Buford Circle, St. Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          μ,
www.medicago.org
Seq primer: (gtA AtA CgA CtC
Location/Qualifiers
                                                                                                                         495 Borlaug Hall,
Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.
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Colletotrichum trifolii
                                                                          Email: debbys@puccini.crl.umn.
TIGR sequence name: MTSAB07TV
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/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript SK+; Site 1: EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
EcoRI; isolate: 2sp2; cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
recombinants."
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/lab_host="DH5alpha"
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DSCT Colletotrichum
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Pred. No. 2.4e-24;
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m trifolii cDNA clone pDSCT2-7, mRNA
                                                                          More information
                                                                                                                                                                                                                                                                                                                                                                             Van Aken, S., Utterback, T.,
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KEYWORDS
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LOCUS
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      Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper I
                                                                                              Unpublished (2002)
Other_ESTs: EST632046
                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoracea mitosporic Phyllachoraceae; Colletotrichum.
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EST632047
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                                                                                                                                       Cheung, F. and Fraser, C.M. ESTs from mycelia of Colletotrichum
                                                                                                                                                                                  Samac, D.A., Dickman, M.,
                                                                                                                                                                                                                                                                                              Colletotrichum trifolii
                                                                                                                                                                                                                                                                                                                                                              BQ751484.1 GI:21906889
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/lab_host="DH5alpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Colletotrichum trifolii"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="mycelia"
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Pred. No. 2.5e-24;
                                                                                                                                                                              Town, C.D., Van Aken, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                          bp mRNA linear
m trifolii cDNA clone
         Buford
      Circle,
                                                                                                                                       trifolii race
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      Paul,
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      55108,
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                                                                                                                                                                                                                                                                                     RESULT 11
BQ751971
LOCUS
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VERSION
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ORGANISM
                                                REFERENCE
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                                                                                                                                                                           sequence.
BQ751971
BQ751971.1
BQ751971.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210;
                    Colletotrichum trifolii
Colletotrichum trifolii
Colletotrichum trifolii
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sc
Sordariomycetes incertae sedis; Phyllachorales;
mitosporic Phyllachoraceae; Colletotrichum.

1 (bases 1 to 745)
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S.,
Cheung, F.
                                                                                                                                                                                                                                                                BQ751971 745 \\ EST632534 DSCT Colletotrichum
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Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAE48TV More
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Location/Qualifiers
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/clome lib="DSCT"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: FBLUESCRI; Solate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coll Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coll DH5alpha which
were plated onto medium with X-gal for selection of
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/dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab_host="pH5alpha"
/clone_lib="DH5CT"
and Fraser, C.M.
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/strain="race 1"
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                                                                                                                                                                                                GI:21907376
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74.2%;
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Pred. No. 2.5e-24;
0; Mismatches 58
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m trifolii
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A clone
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15;

60

170

Sordariomycetes; ' s; Phyllachoraceae;

EST 18-JUL-2002 pDSCT9-3, mRNA

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Colletotrichum trifolii
Colletotrichum trifolii
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TIGR sequence name: MTSAIO3TV More information is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 612 625 1243 Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2002)
Contact: Deborah A. Samac
                                                           BQ751399.1
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/clone lib="DSCT"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquote of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
recombinants."
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inoculation) grown in liquid culture (cutin minimal medium
containing 2%glucose)."
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Location/Qualifiers
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tissue_type="mycelia"
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                                                           GI:21906804
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                                                                                                                     Colletotrichum
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Pred. No. 7.2e-24;
0; Mismatches 59
                                                                                                                 758 bp mRNA linear EST 18-JUL-2002 chum trifolii cDNA clone pDSCT4-95, mRNA
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Pax: 651 649 5058
Email: debbye@puccini.crl.umn.
TIGR sequence name: MTSAD95TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 758)
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utt. Cheung, F. and Fraser, C.M.
ESTs from mycelia of Colletotrichum trifolii race 1 Unpublished (2002)
Other_ESTs: EST631961
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CAAGGTTGACCTCGGATCAGGTAGGAATACCCCGCTGAACTTAA
                             GAATGTTGACCTCGGATCAGGTAGGAATACCCGCTGAACTTAA 310
                                                                                                 ACATACCACCTCGCACCGGGACCCGCAGGGCACTCCTGCCGTAAAACCCCCCCAATTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTGAATCATCGAATCTTTGAACGCACATTGCGCCCGCCAGTATTCTGGCGGGCATGCCT
                                                                                                                                                 GTAAAACCCTCGCAACTGGTA--CGCGGCGCGCCAAGCCGTTAAACCCCCAACTTCT--
                                                                                                                                                                                                   CGGCTGACGTGGGCCCTCAAAGACAGTGGCGGACCCTCGCGGAGCCTCCTTTGCGTAGTA
                                                                                                                                                                                                                                                  TGCGGCAAGCCGGCCCCGAAATCTAGTGGCGGTCTCGC-TGCAGCTTCCATTGCGTAGTA 211
                                                                                                                                                                                                                                                                                                       GTTCGAGCGTCATTTCAACCCTCAAGCACC-
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                                                                                                                                                                                                                                                                                                                                                                                                        AGTGATTCATCGAATCTTTGAACGCACATTGCGCCCGCCAGCATTCTGGCGGGCATGCCT
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/clone lib="DSCT"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
recombinants."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="mycelia"
/dev stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab_host="DH5alpha"
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/strain="race 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 118.6; DB 1
Pred. No. 7.3e-24;
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On Mar 7, 2002 this sequence version replaced gi:19237974.
On Mar 7, 2002 this sequence version replaced gi:19237974.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) gb|AAL79278.1| unknown
[Saccharomyces cerevisiae] 79 1e-14
159
                                                121 CCCG 124
                                                                                                                                                                                                                                                                                           119;
                                                                                                                     61 TIGCGCCCGCCAGTATICTGGCGGGCAIGCCTGTTCGAGCGTCATITCAACCCTCAAGCC 120
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                                                                                                                                                                                                                 1 AAATGCGATAAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA
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BM870292
BM870292.2 GI:30404719
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Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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TCGG 162
                                                                                         TTGCGCCCGCCGGTATTCCGGCGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                              /cell type="mycellum"
/cell type="mycellum"
/clone lib="Magnaporthe grisea NS Uni-Zap XR Library"
/clone lib="Magnaporthe grisea NS Uni-Zap XR Library"
/note="vector: pBluescriptSK: Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Nitrogen starvation library. Cells were inoculated into
minimal medium and grown for two days with shaking (150
rpm) at room temperature. Culture was harvested, blended,
inoculated into minimal medium as above for 24 h. Cells
were harvested, washed with water and inoculated into
minimal medium base lacking nitrogen source for 6 h.
Sequences were processed by one of two methods. Where a
full-length alignment to the M. grisea genome sequence was
available, the EST sequence was trimed according to the
alignment, otherwise sequence quality was assessed using
phredPhrap version 991019 and trimmed according to phd
files (0.05) and for vector seqs."
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/mol_type="mRNA"
/strain="Guy11"
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Pred. No. 2e-23;
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Other_ESTs: EST632698
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ESTs from mycelia of Colletotrichum trifolii race 1
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Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper 1
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Colletotrichum trifolii
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TIGR sequence name: MTSAJ23TV More information
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Fax: 651 649 5058
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                                                                                                                                                   AGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTTGGGGATCGGCAAGCCCTTGCGG 157
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/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtl1 from
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An aliquot of the amplified library was used to transduce
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lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coll DH5alpha which
were plated onto medium with X-gal for selection of
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/lab_host="DH5alpha"
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/clone="pDSCT10-23"
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|strain="race 1"
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73.4%;
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Pred. No. 2.2e-22;
0; Mismatches 59;
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Qy	Db	\$	Query Ma Best Loc Matches	ORIGIN				FEATURES source			TITLE JOURNAL COMMENT	REFERENCE AUTHORS	SOURCE	ACCESSION VERSION KEYWORDS	RESULT 15 BQ751027 LOCUS DEFINITION	Qy Db	B 8
98 AGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTTGGGGGATCGGCAAGCCCTTGCGG 157	5 ATTITCGAATCTITGAACGCACATTGCGCCCGCCAGCATTCTGGCGGGCATGCCTGTTCG 64	38 ATCATCGAATCTITGAACGCACATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCG 97	y Match 36.1%; Score 112; DB 13; Length 743; : Local Similarity 73.0%; Pred. No. 6.3e-22; :hes 203; Conservative 0; Mismatches 60; Indels 15; Gaps 4;	recombinants."	ECORI, isolates 1892; cDNA was prepared from polyA+ enriched RNA The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript Sk+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of	<pre>/tissue_type="mycelia" /dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)." /lab_host="DHSalpha" /clone_lib="DSCT"</pre>	/organism="Collectrichum Erifolii" /mol_type="mRNA" /strain="race 1" /db_xref="taxon:5466" /clone="pDSCT2-20"	Seg primer: (gth AtA CgA CtC ACt At Location/Qualifiers 1743	Fax: 61 649 5058 Email: debbys@puccini.crl.umn.edu TIGR sequence name: MTSAB20TV More information is available at: www.mediago.org	Contact: Deborah A. Samac Department of Plant Pathology University of Minnesota 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA	Cheungyr. and reaser, c.m. ESTS from mycella of Colletotrichum trifolii race 1 Unpublished (2002) Other_ESTs: EST631589	mitosporic Phyllachoraceae; Colletotrichum. 1 (bases 1 to 743) Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T., Chouse E and Expanse M.	COlletotrichum trifolii ISM Colletotrichum trifolii ISM Colletotrichum trifolii Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis: Dhyllachorales Dhyllachoraceae.	sequence. 80751027 B0751027.1 GI:21906432 EST	BQ751027 743 bp mRNA linear EST 18-JUL-2002 EST631590 DSCT Colletotrichum trifolii cDNA clone pDSCT2-20, mRNA	273 TTGACCTCGGATCAGGTAGGAATACCCGCTGAACTTAA 310 	217 ACCCTCGCAACTGGTACGCGGCGGCGAAGCCGGTTAAACCCCCCAACTTCTGAATG 272 175 CCACCTCGCACCGGGACCCGCAGGGCACTCCTGCCGTAAAACCCCCCCAATTTTTACAAGG 234

Search completed: October 1, 2004, 08:01:36 Job time: 4343.33 secs

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Minimum
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1164953

Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	RESULT 1 AR206401 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS		4.5	43	4 3 1	40 40	3 B	37 37	. w .	ມູນ	32	30	29	27	ಬ 5 5	24	22	21	209	18	176	15	: 13	12	: 10	νο α	7	თ თ	44.1	ω N ,		No. S
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fujikuroi complex.
1 (bases 1 to 310)
1 (bases 1 to 310)
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.
Mucleic acids for detecting Aspergillus species and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gibberella fujikuroi
Gibberella fujikuroi
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
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/organism="Gibberella fujikuroi"
/mol_type="genomic DNA"
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Choi,J.S., Westerman,J.M. and Morrison,C.J.
Rapid differentiation of filamentous fungi using species-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibberella fujikuroi
Gibberella fujikuroi
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                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-SEP-1998) DBMD, CDC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA probes
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2 (bases 1 to 310)
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                                                                                                                                                                                                                                       /organism="Gibberella fujikuroi"
/mol_type="genomic DNA"
/strain="ATCC 38519"
/db_xref="ATCC:38519"
                                                                                                                                                      /product="5.8S ribosomal RNA"
159. .272
                                                                 product="28S
                                                                                                         'note="ITS2"
                                                                                                                                                                                                                 db_xref="taxon:5127"
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                            GGCCAAGCCGTTAAACCCCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCG
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Pred. No. 2.7e-171;
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AP117922 JIO bp DNA linear PLN i Gibberella fujikuroi ATCC 38519 5.88 ribosomal RNA gene, sequence; internal transcribed spacer 2, complete sequence ribosomal RNA gene, partial sequence. complete sequence; PLN 17-JUN-2000 partial

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Nectriaceae; (; Sordariomycetes; Gibberella; Gibbe Gibberella

1600 Clifton Rd., Atlanta, GA

spacer

Length 310;

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AP162903
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Fusarium proliferatum
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
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                                                                                                                                                                                                                                                                                       Submitted (28-JUN-1999) Biology, SangMyung Dong, Chong Ro-Gu, Seoul 110-743, Korea
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                                                                                                                                                                                                                                                                                                                                 fujikuroi complex.
1 (bases 1 to 351)
                                                                                                            Similarity
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                        TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTTGGGGAA
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                              Submission
                                                                                                                                                                                                                               /organism="Fusarium proliferatum"
/mol_type="genomic DNA"
/strain="6787"
                                                                                                                                                                /product="internal transcribed 294. .>351
                                                                                                                                                                                      /product="5.8S ribosomal 129. .293
                                                                                                                                                     product="28S ribosomal
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                                                                                               Score 232; DB 8; Pred. No. 3.4e-125; 0; Mismatches 1;
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (04-DEC-2001) Laboratory for Mycology and Molecular Biology, ENT-University Hospital, Auenbruggerplatz 26-28, Graz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stammberger, H.
Direct Submission
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Buzina, W., Braun, H.,
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Buzina, W., Braun, H., Freudenschuss, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibberella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tujikuroi
                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                     AGTAGTAAAACCCTCGCAACTGGTACGCGGCGCGCGAGCCGTTAAACCCCCCAACTTCT
GCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTGGCGGTCTCGCTGCAGCTTCCATTGCGT
                           GCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTGGCGGTCTCGCTGCAGCTTCCATTGCGT
                                                                                                        TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTTGGGGATCGGCAA
                                                                                                                                                               GAATGTTGACCTCGGATCAGGTAGGAATACCCGCTGAACTTAA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATGTTGACCTCGGATCAGGTAGGAATACCCGCTGAACTTAA 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Austria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="small
49. .247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:5127"
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                                                                                                                                                                                                                                                                                                                                                  'product="large
                                                                                                                                                                                                                                                                                                                                                                                           product="internal transcribed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'mol_type="genomic DNA"
'isolate="wb518"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Gibberella fujikuroi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   product="5.8S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="internal transcribed spacer 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fujikuroi (anamorph: Fusarium fujikuroi)
fujikuroi
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                                                                                                                                                                                                                                                               74.8%;
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149-161 (2003)
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                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                               Score 232; DB 8;
Pred. No. 3.4e-125;
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                                                                                                                                                                                                                                                                                                                                                     ribosomal
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                                                                                                                                                                                                                                                                                                                                                                                         spacer
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AF455460
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Best Local Similarity
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                                                                     148 GCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTGGCGGTCTCGCTGCAGCTTCCATTGCGT
                                                                                                                                                                              454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AP455460 556 bp DNA linear PLN 16-JUN-20 Gibberella fujikuroi isolate wb355 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.88 ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibberella fujikuroi (anamorph: Fusarium fujikuroi)
Gibberella fujikuroi
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomyc
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-DEC-2001)
Biology, ENT-University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buzina,W., Braun,H., Freudenschuss,K.,
Stammberger,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 556)
Buzina, W., Braun, H., Freudenschuss, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stammberger, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fungal biodiversity
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AGTAGTAAAACCCTCGCAACTGGTACGCGGCGCGCCCAAGCCGTTAAACCCCCCAACTTCT
                                                                                                               TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTGGGGGATCGGCGA
                                                                                                                                 TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTTGGGGATCGGCAA
                                                                                                                                                                                                AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCGGCCAGTATTCTGGCGGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 556)
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                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                         /product="internal transcribed spacer 2"
519. .>556
                                                                                                                                                                                                                                                                                                                        /product="large subunit ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="small subunit ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:5127"
                                                                                                                                                                                                                                                                                                                                                                                         /product="5.8S ribosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Gibberella fujikuroi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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isolate="wb355"
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99.6%;
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149-161 (2003)
                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                            Score 232; DB 8;
Pred. No. 3.4e-125;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                         RNA"
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                                                                                                                                                                                                                                             1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     spacer 1"
                                                                                                                                                                                                                                                                        Length 556
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Gibberella; Gibberella
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VERSION
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Best Local S
Matches 282
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Gibberella fujikuroi (anamorph: Fusarium fujikuroi)
Gibberella fujikuroi
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-DEC-1995) C. Waalwijk, Research Inst. for Pl Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS On Jun 15, 2001 this sequence version replaced gi:1103564. Overlaps with X78260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waalwijk,C., de Koning,J.R.A., Baayen,R.P. and Gams,W. Discordant groupings of Fusarium spp. from sections Elegans, Liseola and Dlaminia a based on ribosomal ITS1 and ITS2 sequence Mycologia 88, 361-368 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFUJERNA 558 bp DNA linear PLN 14-JUN-7 PLN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waalwijk,
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                                                                                                                                                                                                                                                                                          Similarity
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TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTTGGGGATCGGCAA 147
                                                                                                             AATTCAGIGAATCATCGAATCTTIGAACGCACATTGCGCCCGCCAGTATTCTGGCGGGCA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTAGTAAAACCCCTCGCAACTGGTACGCGGCGGCGGCCAAGCCGTTAAACCCCCCAACTTCT 513
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol type="genomic DNA"
/strain="CBS 221.76"
/specific hoor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="5.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="5.8 rRNA"
178. .335
                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="28S rRNA"
product="28S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="28S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="internal transcribed spacer 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="18S rRNA"
/product="18S ribosomal
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99.6%;
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Pred. No. 3.4e-125;
0; Mismatches 1;
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Submitted (08-DEC-1995) C. Waalwijk, Research I Submitted (08-DEC-1995) C. Waalwijk, Research I Protection, PO box 9060, 6700 GW Wageningen, NE On Jun 15, 2001 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.
Fusarium proliferatum
Fusarium proliferatum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waalwijk,C., de Koning,J.R.A., Baayen,R.P. and Gams,W. Discordant groupings of Fusarium spp. from sections Elegans, Liseola and Dlaminia a based on ribosomal ITS1 and ITS2 sequence Mycologia 88, 361-368 (1996)

2 (bases 1 to 558)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPRORRNA 558 bp DNA linear PLN 14-JUN-2001 Fusarium proliferatum 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Overlaps with X78260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waalwijk, C.
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                                                                                               /gene="28S rRNA"
501. .>558
                                                                                                                                                             /gene="5.8 rRNA"
/product="5.8 ri
336. .500
                                                                                                                                                                                                                                                                                          /gene="18S rRNA"
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/product="28S ri]
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178. .335
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                                                                                                                                              note="internal transcribed"
                                                                                                                                                                                                                                                                                                                                          'gene="18S
                                                                                                                                                                                                                                                           note="internal transcribed spacer 1,
                                                                                                                                                                                                                                                                                                                                                                        specific_host="Cattleya"
db_xref="taxon:42674"
                                                                                                                                                                                                                                                                                                                                                                                                        mol_type="genomic DNA"
strain="CBS 217.76"
                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Fusarium proliferatum"
   74.8%;
99.6%;
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No. 3.4e-125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusarium sp. 03001
Fusarium sp. 03001
Eusaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 562)
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AY237110

Solve DNA linear PLN 09-APR-200: Fusarium sp. 03001 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8 ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

AY237110

AY237110
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                                                                                                                                                                               Similarity
                                                                                              GCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTGGCGGTCTCGCTGCAGCTTCCATTGCGT
                                                   TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTGGGGGATCGGCAA
                                                                                                                          TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTGGGGGATCGGCGA
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                                                                                                                                                                                                                                                                                                                                  /product="internal transcribed
187. .345
                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:227081"
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Fusarium sp. 03001"
/mol_type="genomic DNA"
/isolate="03001"
                                                                                                                                                                                                                                                 /product="28S ribosomal
                                                                                                                                                                                                                                                                                /product="internal transcribed
                                                                                                                                                                                                                                                                                                                 product="5.8 ribosomal RNA"
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                                                                                                                                                              Score 232; DB 8;
Pred. No. 3.4e-125;
0; Mismatches 1;
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Best Local Similarity
Matches 282; Conserv
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    AF291061
Fusarium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pythium ultimum var. sporangiiferum RNA gene, partial sequence.
AF452163.1 GI:17980882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26-NOV-2001) Plant Patholo University, 210 Buckhout Laboratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 569)
Moorman,G.W., Geiser,D.M., Kang,S. and Kim,S.
Pythium species and a population identification uppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pythium ultimum var. sporangiiferum
Pythium ultimum var. sporangiiferum
Eukaryota; stramenopiles; Oomycetes; Pythiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                        AGTAGTAAAACCCTCGCAACTGGTACGCGGCGGCGCCAAGCCGTTAAACCCCCCAACTTCT
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llarity 99.6%;
Conservative
   596 bp DNA linear proliferatum NRRL 31071 18S ribosomal RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pythium ultimum
/mol_type="genomic DNA"
/variety="sporangiiferum"
/isolate="308276R"
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Pred. No. 3.4e-125;
0; Mismatches 1;
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ratory, University
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                                                                                                           Sequence
AR168094
1 (bases 1 to 2293)
Gallazzo, J. L. and Lee, M.D.
Production of high titers of gibberellins,
Gibberella fujikuroi strain LTB-1027
                                                 Unknown.
Unclassified
                                                                          Unknown
                                                                                                 AR168094.1
                                                                                                                                    AR168094
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /specific_host="Triticu
/db_xref="taxon:42674"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Fusarium pro
/mol_type="genomic DNA"
/strain="NRRL 31071"
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99.6%;
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patent US 6287800.
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Gene sequence analysis of an opportionate of Fusarium proliferatum Can. J. Bot. 79 (9), 1115-1121 (20) 2 (bases 1 to 596) Kwon, S.-I. and Anderson, A.J. Direct Submission Submitted (31-JUL-2000) Biology, University of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence; internal transcribed spacer 1, 5.8S ribosomal RNA, and internal transcribed spacer 2, complete sequence; 28s ribosomal RNA, partial sequence.

AF291061

AF291061.1 GI:15637128
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreomycetidae, Hypocreales; Nectriaceae;
                                                                                                                                                                                                                                                                                             GAATGTTGACCTCGGATCAGGTAGGAATACCCGCTGAACTTAA 310
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spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, 28S ribosomal RNA"
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Pred. No. 3.4e-125;
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n opportunistic
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                                                                                                                                                                                                           O'Donnell,K., Cigeinik,E. and Nirenberg,H.I.
Molecular systematics and phylogeography of the
fujikuroi species complex
Mycologia 90 (3), 465-493 (1998)
3 (bases 1 to 534)
O'Donnell,K. and Cigelnik,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusarium fujikuroi internal transcribed spacer RNA.
                                                                                                                                                      Submitted (21-AUG-1995) Kerry O'Donnell, University St., Peoria, IL 61604, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           Two divergent intragenomic rDNA ITS2 types within lineage of the fungus Fusarium are nonorthologous Mol. Phylogenet. Evol. 7 (1), 103-116 (1997)
                                                                                                                                                                                                                                                                                                                                                                                      O'Donnell, K. and Cigelnik, E.
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
                                                                                                                                                                                                  Direct Submission
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1 (bases 1 to 534)
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Location/Qualifiers
                                                                                                /organism="Gibberella fujikuroi"
/mol_type="genomic DNA"
/strain="NRRL 13566"
                                                       /product="internal transcribed spacer"
                                                                              db_xref="taxon:5127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unknown"
/mol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                              fujikuroi
fujikuroi
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99.6%;
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Pred. No. 3.6e-125;
0; Mismatches 1;
 Score 228; DB 8;
Pred. No. 7.9e-123;
              Length
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U34558
                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (21-AUG-1995) Kerry O'Donnell,
University St., Peoria, IL 61604, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 534)
O'Donnell, K. Cigelnik, E. and Nirenberg, H.I.
O'Donnell, K. Cigelnik, E. and phylogeography of
fujikuroi species complex
Mycologia 90 (3), 465-493 (1998)
3 (Dases 1 to 534)
O'Donnell, K. and Cigelnik, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 534)
O'Donnell,K. and Cigelnik,E.
O'Dondell,K. and Cigelnik,E.
Two divergent intragenomic rDNA ITS2 types within lineage of the fungus Fusarium are nonorthologous Mol. Phylogenet. Evol. 7 (1), 103-116 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pusarium proliferatum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
                                                                                                                                    Similarity
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                 TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTTGGGGATCGGCAA 147
                                                                           GAATGTTGACCTCGGATCAGGTAGGAATACCCGCTGAAC
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TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTGGGGATCGGCGA
                                                          AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCGCCAGTATTCTGGCGGGCA
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                                                                                                                                                                                              1. .534
/product="internal transcribed spacer"
                                                                                                                                                                                                                                        organism="Fusarium pro/mol_type="genomic DNA"/strain="NRRL 22944"
                                                                                                                                                                                                                             db_xref="taxon:42674"
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208 AGTAGTAAAACCCTCGCAACTGGTACGCGGCGCGCCAAGC
208 ACTAGTAAAACCCTCGCAACTGGTACGCGGCGCGGCGGCGGCGTTAAACCCCCAACTTCT 267

Search completed: October 1, 2004, 09:56:24 Job time : 1578.63 secs

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Database
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310
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ALIGNMENTS

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22310 53340 53340 55340 55360 55360 55360 55360 55360 55360 55360 55360 55360 55360 55360 55360	Length
04 L M B B O O O O O O O O O O O O O O O O O	DB
	SUMMARIES
Aav70851 Internal Aas16211 Fungus ge Acc50001 Internal Aaa61893 Fusarium Abv78700 C. crassi Abv78721 C. sinens Aat05400 Fusarium Aav62591 Fusarium Aav62591 Fusarium Aav59028 F. culmor Aas08426 Internal Acc50000 Internal Acc50000 Internal Acc50002 Internal Acc50007 F. monili Aav62593 Fusarium Aav59030 F. monili Aav62596 Fusarium Aav59030 F. soae i Aaa72783 5.8s rRNA Aaf10640 Fusarium Aav70850 Internal Aax10640 Rhizocton Aat65101 T. harzia Aat65099 T. harzia	Description

The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species-specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from

Claim 1; Page 12; 45pp; English.

New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothr

Sporothrix

WPI; 1999-034737/03.

Morrison CJ,

Reiss E,

Aidorevich L, Choi JS;

(USSH) US DEPT HEALTH & HUMAN SERVICES.

02-MAY-1997; 01-MAY-1998;

97US-0045400P. 98WO-US008926. 12-NOV-1998.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	4.7
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Aca62941	Ada27221	Aaz22436	Aaf75170	Aaf75169	Aaa72781	Aba94560	Aba94561	Aba94564	Aba 94559	Aaz91726	Aav70870	Aav70871	Aaz91725	Aat05403	Aav59029	Aav62592	Aat05401	Aat05402	Abv78724	Aav59009	Macaston
P. glomer	P. micros	Internal	Consensus	Consensus	5.88 rRNA	Truncated	Truncated	Consensus	Truncated	Rosellini	Internal	Internal	Rosellini	Microdoch	F. gramin	Fusarium	Fusarium	Fusarium	C. sinens	F. avenac	T. Marara

RESULT 1 AAV70851 ID AAV7 XX Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; A. terreus; M. plumbeus; M. indicus; A. funigatus; M. carcinilloides f. circinelloides; Rhizopus oryzae; R. microsporus; R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum; Penicillium notatum; Sporothrix schenkii; filamentous fungus; ss. AAV70851; WO9850584-A2. Gibberella fujikuroi. 17-OCT-2003 26-FEB-1999 AAV70851 standard; DNA; 310 Internal transcribed spacer 2 (ITS2) and adjacent regions. (revised) (first entry) ВP

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RESULT 2
AAS16211
ID AAS1
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XX AAS1
XX Gibb
XX Gibb
XX Gibb
XX FIOW
XX F
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                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                           /note= "18S rRNA gene"
1775. .1921
                                                                                                                          /note= "5.8S rRNA gene"
2079. .2243
                                /note= "ITS2 region"
2244. .2293
                                                                                                                                                                                                                    /note= "ITS1 region"
1922. .2078
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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ered. No. 2.5e-154;
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RESULT 3
ACC50001
ID ACC5
XX
AC ACC5
XX
DT 14-J
XX
Inte

ACC50001 standard; DNA; 534

14-JUL-2003

(first entry)

Internal transcribed spacer RNA encoding sequence #3.

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Best Local Simi
Matches 282;
                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a genomic DNA sequence containing the 18S rRNA gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S rRNA sequences from a mutant strain of Gibberella fukikoroi (LIB-1027) of the invention. This region of DNA is highly variable and can be used for species and strain differentiation. The LIB-1027 mutant produces a mixture of gibberellins which is at least 70 % GA 4 and GA 7. Gibberellins GA 4 and GA 7 promotte flowering and Fruit cell elongation, and are used by growers of apples, pears and grapes to produce larger fruits and earlier harvests. The mixture of GA 3, GA 4 and GA 7 achieved using the method of this invention should be particularly useful in the apple industry where GA 4 has been found more effective in russet control and in promoting fruit set. This method produces GA 4 and GA 7 in much higher titers than prior art methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new method for producing a mixture of gibberellins from fujikuroi results in high titers of GA4 and GA7 useful to flowering and fruit growth in the fruit growing industry.
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Col 9-12; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-662197/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallazzo JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6287800-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GALL/) GALLAZZO J L. (LEEM/) LEE M D.
                                                               2179
 2239
                                                                                                                                2119
                                                                                                                                                                                               2059
                                                                                                                                                                                                                                                              1999
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                                                                                               208
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                                                                                                                                                                                                                                                                                                                                               Similarity
                      GAATGTTGACCTCGGATCAGGTAGGAATACCCGCTGAACTTAA 310
                                                                                                                                                 GCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTGGCGGTCTCGCTGCAGCTTCCATTGCGT 207
                                                                                                                                                                                                                TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTGGGGGATCGGCAA 147
                                                                                                                                                                                                                                                             GAATGTTGACCTCGGATCAGGTAGGAATACCCGCTGAACTTAA 2281
                                                               AGTAGTAAAACCCTCGCAACTGGTACGCGGCGGCGAAGCCGTTAAACCCCCAACTTCT
                                                                                            AGTAGTAAAACCCTCGCAACTGGTACGCGGCGGCGGCCAAGCCGTTAAACCCCCCAACTTCT 267
                                                                                                                                                                                            TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTGGGGATCGGCGA
                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                          74.8%;
99.6%;
                                                                                                                                                                                                                                                                                                                          Score 232; DB 4; 1
Pred. No. 6.4e-113;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                           Length 2293;
                                                                                                                                                                                                                                                                                                                                                                                           U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods and primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present sequence represents an internal transcribed spacer RNA encoding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469; HIV integrase inhibitor; steroid compound; human immunodeficency virus; acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;
                                                                           15-SEP-2003
14-NOV-2000
                                                                                                                                        AAA61893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 38-39; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beck JJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusarium spp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.5%;
Similarity 99.6%;
                                                   sp.
                                                                                                                                        standard; DNA;
                                                                                                                                                                                                     GAATGITGACCICGGATCAGGTAGGAATACCCGCTGAAC 534
                                                                                                                                                                                                                       GAATGTTGACCTCGGATCAGGTAGGAATACCCGCTGAAC
                                                                                                                                                                                                                                                                                                                                                          TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTTGGGGATCGGCGA
                                                                                                                                                                                                                                                        AGTAGTAAAACCCTCGCAACTGGTACGCGGCGGCCAAGCCGTTAAAACCCCCCAACTTCT
                                                                                                                                                                                                                                                                         AGTAGTAAAACCCTCGCAACTGGTACGCGGCGGCGGCCAAGCCGTTAAACCCCCCAACTTCT
                                                                                                                                                                                                                                                                                                                                GCCCTTGCGGCAAGCCGGCCCCGAAATCTAGTGGCGGTCTCGCTGCAGCTTCCATTGCGT
                                                                                                                                                                                                                                                                                                                                                                                  TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGGTTTGGTGTTGGGGATCGGCAA 147
                                                                                                                                                                                                                                                                                                                                                                                                          534 BP; 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barnett
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                          (revised)
(first ent
                                                MF6381 rDNA internal transcribed spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; 149 C; 130 G; 120 T; 0 U; 0 Other;
                                                                                                                                         502
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Pred. No. 8.
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                                                   (STI)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel steroid compounds derived from the African CC soil fungus Fusarium sp. MF6381 (ATCC 74469) which act as inhibitors of CC HIV integrase. The invention encompasses cultures of Fusarium sp. MF6381. CC The invention also relates to a composition comprising a compound of the invention in combination with an AIDS antiviral agent, an immunomodulator CC and an antiinfective agent. The compounds of the invention may be used in the inhibition of HIV integrase and in the prevention and treatment of CC HIV infection. A wide range of state of HIV infection may be treated: CC AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex); CC both symptomatic and asymptomatic HIV infection; and actual or potential CC exposure to HIV. The compounds may be used to isolate HIV integrase CC mutants which are potentially useful as screening tools for antiviral CC compounds. The compounds may also be used to establish or determine the cite at which other antivirals bind to HIV integrase (e.g., by CC competitive inhibition). The present sequence represents the ribosomal CC MF6381, which may be used to characterise MF6381. (Updated on 15-SEP-2003 CC to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                    ABV78700;
                                                 Cordyceps sinensis; ss.
                                                                               Ribosome ribonucleic acid;
                                                                                                                                                                                     14-JAN-2003
                                                                                                                                                                                                                                                                                           ABV78700 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New steroid compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-431606/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Singh SB,
Dombrowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERI ) MERCK & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-DEC-1998;
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                                                                                                                              crassispora rRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recordinocado en carriro da como concese de construcción de co
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCTGTTCGAGCGTCATTTCAACCCCTCAAGCCCCCGGGTTTGGTGTTTGGGGATCGG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zink
AW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP;
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0112168P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 A; 144 C; 118 G; 113
                                                                                                                                                                                                                                                                                           rRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hazuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are HIV integrase inhibitors
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                                                                             rRNA; Cordyceps
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                                                                               crassispora;
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                                                                               classification;
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Cordyceps crassispora

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RESULT 6
ABV78721
ID 78721
XX ABV7
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Best Local :
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                               Ribosome RNA gene base sequence of Cordyceps sinensis for classification of seeds of Cordyceps sinensis.
                                                                                      (KANE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel base sequence which is part of a fully defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispora. The base sequences can be used for the classification of Cordyceps sinensis. The sequence represents a C. crassispora rRNA sequence of the
                                                                 WPI;
                                                                                                                    12-JAN-2001; 2001JP-00004805
                                                                                                                                         12-JAN-2001;
                                                                                                                                                                                   JP2002204696-A
                                                                                                                                                                                                        Cordyceps sinensis.
                                                                                                                                                                                                                             Cordyceps sinensis;
                                                                                                                                                                                                                                        Ribosome ribonucleic
                                                                                                                                                                                                                                                            C. sinensis rRNA sequence #20
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                                                                                                                                                                                                                                                                                                                            ABV78721 standard; rRNA; 661 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Page 12; 33pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-639075/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seeds
                                                               2002-639075/69
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                                                                                     HEALTHWAY KK
KANESHIRO N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEALTHWAY KK
KANESHIRO N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         647 BP; 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA gene base sequence of Cordyceps sinensis for classification of Cordyceps sinensis.
                                                                                                                                                                                                                                                                                                                                                                               TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                           2001JP-00004805
                                                                                                                                                                                                                                                                                  (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.2.
100.0%; rr
                                                                                                                                                                                                                                      acid; rRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 178 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 99;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                      Cordyceps crassispora; classification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 T; 0 U;
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hes 0;
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23; Page

24; 33pp; Japanese

Query Match

30.3%;

Score

94;

В

2

Length 504;

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Matches
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Best Local
                        A novel method for the detection of plant pathogenic strains of fungi e.g. Septoria nodorum, S.tritici, Pseudocercosporella herpotrichoides, Mycosphaerella fijiensis, M. musicola or Rusarium spp. involves the PCR amplification of sequences found in the internal transcribed region (ITS) of the 185, 5.85 and 285 ribosomal RNA genes by the primers AAQ94359-93 and AAT05357-72. These primers are derived from the ITS sequences of these fungi (AAT05394-T05404 and AAQ94398) and are strain specific. The amplification products of the reactions using these primers can be used with the capture primers AAT05378-93 in colourimetric assays. The primers and ITS DNAs can be used for the detection of specific fungal pathogen isolates and in monitoring disease development in plant populations
 Sequence
                                                                                                                                                                                                       Claim 1; Page 54-55; 65pp;
                                                                                                                                                                                                                                                                                 WPI; 1995-383005/49
                                                                                                                                                                                                                                                                                                             Ligon JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusariu
Pseudocercosporella herpotrichoides; Mycosphaerella fijiensis; PCR;
Mycosphaerella musicola; amplification; primer; ribosomal RNA gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 661 BP; 176 A; 192 C; 168 G; 123 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispo: The base sequences can be used for the classification of Cordyceps sinensis. The sequence represents a C. sinensis rRNA sequence of the
                                                                                                                                                                                                                                                                                                                                          (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                       25-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                  19-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                               02-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9529260-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusarium culmorum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusarium culmorum internal transcribed spacer sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT05400 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel base sequence which is part of a fully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isolate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                    encoding intervening transcribed sequence - nt fungal pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCGCCAGTATTCTGGCGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
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   504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   development;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcribed region;
                                                                                                                                                                                                                                                                                                             Beck JJ;
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   BP; 133
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 A; 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504
                                                                                                                                                                                                       English.
 C; 113
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain; capture; colourimetric
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 122 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amplified polymorphic DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
   U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 661
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This represents the consensus DNA sequence of the internal transcribed spacer (ITS) region that was PCR amplified from Fusarium culmorum isolates, R-5106, R-5126 and R-5146. The invention provides a DNA molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal pathogen, where the DNA molecule consists of an ITS sequence selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium moniliforme, Septoria avenae or Microdochicum nivale. A method for
                                                                                                   DNA isolated from fungal RNA, seguence - used for detecting
                                                                                                                                   WPI; 1998-541745/46.
                                                                                                                                                                                            19-APR-1995;
15-OCT-1996;
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                                                                                                                                                                         (NOVS ) NOVARTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusarium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen; culmorum; Fusarium graminearum; Fusarium moniliforme; plant; avenae; Microdochicum nivale; Fusarium poae; Fusarium avenaceu
                                                                               Fig 3; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            culmorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                           95WO-US004712.
96US-00722187.
                                                                                                                                                                                                                                                                                                                                                                                       /note= "3'
13. 161
/*tar
                                                                                                                                                                                                                         97US-00887480
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/note= "5.8S rRNA g
319. .472
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/note= "ITS
162. .318
                                                                                                                                                                                                                                                                                                        473. .504
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                                                                                                                                                                        FINANCE CORF
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; Mismatches 0;
                                                                                                   and its internal fungal pathogens
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                                                                                                                                                                                                                                                                                                                                                                                                         small subunit rRNA gene"
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                                                                                                  transcribed spacer in plant tissue.
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RESULT 9
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This sequence represents an internal transcribed spacer (ITS) sequence the invention. The primer pairs, based on the ITS sequences, are us the PCR amplification detection of wheat Microdothium and Fusarium pathogens, especially M. nivale, F. graminearum, F. culmorum, F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different strains of fungi show different symptoms during infection, which ma may not be due to infection. Early identification of the strain cau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F. avenaceum and M. nivale isolates is also provided. The method comprises isolating DNA from a plant leaf infected with at least one of the above pathogens and amplifying parts of the ITS sequence of the pathogen(s) by PCR using specific primers from within these sequences. The pathogen(s) are detected by visualising the amplified part of the ITS sequence
                                                                                                Disclosure; Col 21-22; 20pp;
                                                                                                                                   Wheat pathogen internal transcribed spacer sequences - used as for primers for the species-specific polymerase chain reaction
                                                                                                                                                                        WPI; 1998-593995/50
                                                                                                                                                                                                Beck JJ;
                                                                                                                                                                                                                                               04-AUG-1997;
                                                                                                                                                                                                                                                                      04-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                     misc_feature
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06-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fungal pathogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                               97US-00905314.
                                                                                                                                                                                                                                                                      97US-00905314.
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                                                                                                                                                                                                                                                                                                                                                                     /note= "ITS1"
319. .472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microdochium; Fusarium; nfection identification;
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                                                                                                                                                                                                                                       The sequence is an internal transcribed spacer (ITS) region from Fusarium culmorum, isolate 62215. The ITS DNA sequences are useful for detecting Rhizoctonia cerealis, a fungal pathogen of wheat causing Sharp eyespot, for monitoring disease development in plant population, and for providing detailed information on the development and spread of specific pathogen races over extended geographical areas. The DNA sequences are specifically used as primers in PCR-based analysis for the identification of fungal pathotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New internal transcribed spacer DNA sequences, useful for identifying fungal pathogen, particularly Rhizoctonia cerealis, and for monitoring disease development in plant population.
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 31; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-2001; 2001WO-EP000172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-442154/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Internal transcribed spacer; ITS; fungal pathogen; ss; wheat disease;
Sharp eyespot; fungal pathotype identification; isolate 62215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Internal transcribed spacer,
                                                                                                                       Local
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                                                                                                                    Similarity
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100.0%; Pr
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100.0%; Pred. No.
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                                                                                         Score 94; DB; Pred. No. 1.3
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                                                                                                                                                                                        123 T;
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                                                                                                                  DB 4; Lo
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods ar primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present sequence represents an internal transcribed spacer RNA encoding sequence
                           Mitochondria;
                                                                                                                                    14-JUL-2003
                                                                                                                                                                                        ACC49999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                             ACC49999
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                                                                          Internal transcribed spacer RNA encoding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-SEP-2001; 2001US-00961755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-SEP-2002; 2002WO-US030311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003027635-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibberella zeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondria; fungal pathogen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Internal transcribed spacer RNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC50000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACC50000 standard; DNA; 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŢŢ,
                                                                                                                                                                                                                                                                                                                                                                              316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302
                                                                                                                                                                                                                                                                                                                                                                                                                             88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 522
                                                                                                                                                                                                                                                                                                                                                                            TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barnett CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.3%; Score 94; ilarity 100.0%; Pred. No. Conservative 0; Mismatcl
                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                              fungal pathogen; ds
                                                                                                                                    entry)
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                                                                                                                                                                                                                                             ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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RESULT 13
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods ar primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present sequence represents an internal transcribed spacer RNA encoding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
         WPI; 2003-363229/34
                            Beck JJ,
                                                                  24-SEP-2001;
                                                                                      19-SEP-2002;
                                                                                                          03-APR-2003
                                                                                                                             WO2003027635-A2.
                                                                                                                                                 Gibberella moniliformis
                                                                                                                                                                   Mitochondria; fungal pathogen;
                                                                                                                                                                                        Internal transcribed
                                                                                                                                                                                                          27-OCT-2003
14-JUL-2003
                                                                                                                                                                                                                                         ACC50002;
                                                                                                                                                                                                                                                          ACC50002 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 522 BP; 138 A; 141 C; 119 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-2001; 2001US-00961755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusarium subglutinans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SYGN)
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                                                                                                                                                                                                                                                                                                             316
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                                                                                                                                                                                                                                                                                                                                88
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                                                                                                                                                                                                                                                                                                                                                                                           94;
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNGENTA PARTICIPATIONS
                                              SYNGENTA
                                                                                                                                                                                                                                                                                                                                                                AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCGCCAGTATTCTGGCGGGCA
                                                                                                                                                                                                                                                                                                             TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC
                                                                                                                                                                                                                                                                                                                                TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC
                                                                                                                                                                                                                                                                                                                                                     Page 38; 44pp; English.
                             Barnett CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barnett CJ;
                                                                                                                                                                                                                                                                                                                                                                                          30.3%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                         (revised)
(first en
                                                                  2001US-00961755
                                                                                      2002WO-US030311
                                              PARTICIPATIONS
                                                                                                                                                                                                          entry)
                                                                                                                                                                                       spacer RNA encoding sequence
                                                                                                                                                                                                                                                           522
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                                                                                                                                                                                                                                                                                                                                                                                          <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                   Score 94;
Pred. No.
                                                                                                                                                                    dB.
                                               ĀG
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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3. 1.3e-39;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                               124 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                            349
                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                           Length 522;
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RESULT 14
AAV62593
ID AAV62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods and primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present sequence represents an internal transcribed spacer RNA encoding sequence. (Updated on 27-OCT-2003 to standardise OS field)
         19-APR-1995;
15-OCT-1996;
                                                                                                                           misc_feature
                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
                                          02-JUL-1997;
                                                              29-SEP-1998
                                                                                    US5814453-A
                                                                                                                                                            misc_feature
                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                               Gibberella fujikuroi
                                                                                                                                                                                                                                                                                                                            Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
Septoria avenae; Microdochicum nivale; Fusarium poae; Fusarium avenaceum;
                                                                                                                                                                                                                                                                                                                                                                         Fusarium moniliforme PCR amplified ITS region DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-2003
17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                AAV62593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV62593
                                                                                                                                                                                                                                                                                                                   PCR; nucleic acid detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                          transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen; culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 39; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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(first entry)
         95WO-US004712.
96US-00722187.
                                          97US-00887480
                                                                                                                                     /*tag= d
/note= "ITS
                                                                                                                                                              336. .488
                                                                                                                                                                                                                                     /note= "3'
                                                                                                         /*tag=
/note=
                                                                                                                              489. .545
                                                                                                                                                                                              179. .335
                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                         note= "5.8S"
                                                                                                                                                                                                         /*tag= b
/note= "ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.3%;
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                                                                                                                                                                                                                                                                                                                   88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 94;
Pred. No.
                                                                                                         of.
                                                                                                                                                                                                                                         of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                         large subunit
                                                                                                                                                                                                                                         small subunit rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 522;
                                                                                                          rRNA
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                                                                                                         gene"
                                                                                                                                                                                                                                       gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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RESULT 15
AAV59030
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This represents the DNA sequence of the internal transcribed spacer (ITS) region that was PCR amplified from Fusarium moniliforme. The invention provides a DNA molecule isolated from the ribosomal RNA gene region of a fungal pathogen, where the DNA molecule consists of an ITS sequence selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium moniliforme, Septoria avenae or Microdochicum nivale. A method for detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F. avenaceum and M. nivale isolates is also provided. The method comprises isolating DNA from a plant leaf infected with at least one of the above pathogens and amplifying parts of the ITS sequence of the pathogen(s) by PCR using specific primers from within these sequences. The pathogen(s) are detected by visualising the amplified part of the ITS sequence. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2003
25-MAR-2003
 04-AUG-1997;
                                   04-AUG-1997;
                                                                     27-OCT-1998.
                                                                                                        US5827695-A.
                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                       Gibberella fujikuroi.
                                                                                                                                                                                                                                                                                                                     Internal transcribed spacer; ITS fungal pathogen identification;
                                                                                                                                                                                                                                                                                                                                                                           F. moniliforme internal transcribed spacer.
                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                               06-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV59030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV59030 standard; DNA; 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA isolated from fungal RNA, sequence - used for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 545 BP; 148 A; 143 C; 125 G; 129 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 3; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCGCCAGTATTCTGGCGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
97US-00905314
                                   97US-00905314
                                                                                                                                        /*tag= a
/note= "ITS1"
336. .488
/*tag= b
/note= "ITS2"
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.3%; Score 94;
100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       묭
                                                                                                                                                                                                                                                                                                                       ITS; Microdochium; Fusarium;
on; infection identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and its internal transcribed spacer fungal pathogens in plant tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3e-39;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                         wheat pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                        This sequence represents an internal transcribed spacer (ITS) sequence of the invention. The primer pairs, based on the ITS sequences, are used for the PCR amplification detection of wheat Microdochium and Fusarium fungal pathogens, especially M. nivale, F. graminearum, F. culmorum, F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different strains of fungi show different symptoms during infection, which may or may not be due to infection. Early identification of the strain causing the infection allows early, and more specific fungicidal treatment. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 55-MAR-2003 to
                                                                                                                                                                                                                                                             Sequence 545 BP; 148 A; 143 C; 125 G; 129 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 23-26; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the pathogens.
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                                                                                     TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC 121
                                                                  TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC
 : October
                                                                                                                                                                                            30.3%; So ilarity 100.0%; I Conservative 0;
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                  2004, 09:02:49
                                                                                                                                                                                                            Score 94;
Pred. No.
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5. 1.3e-39;
0;
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                                                                                                                                                                                                                           Length 545;
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detection
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Result
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length:
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  Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-652-127C-6
US-08-887-480-82
US-08-905-314A-19
US-08-905-314A-21
US-08-905-314A-22
US-08-905-314A-22
US-08-905-314A-24
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US-08-905-314A-24
US-08-652-127C-8
US-08-905-314A-24
US-08-652-127C-8
US-08-652-127C-8
US-08-905-314A-24
US-08-652-127C-8
US-08-722-187-83
US-08-722-187-83
US-08-722-187-83
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(without alignments)
3356.386 Million cell update
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US-09-423-233-7
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Best Local
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US-08-887-480-1	US-08-233-608-1	PCT-US95-04712-6	US-08-722-187-6	US-08-887-480-6	US-08-233-608-6	US-09-517-790-5	PCT-US95-04712-5	US-08-722-187-5	US-08-887-480-5	US-08-233-608-5	US-09-481-293-33	1	US-09-517-790-2	บร-09-517-790-1	US-09-037-990B-5	US-09-635-747-40	US-09-635-747-39
Sequence 1, A	Sequence 1, A	Sequence 6, A	e 6,	Sequence 6, A	Sequence 6, A	Sequence 5, A	Sequence 5, A	o u	Sequence 5, A	'n	Sequence 33, i	Sequence 4, A	Sequence 2, A	e 1,	Sequence 5, A	Sequence 40,	Sequence 39,
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ALIGNMENTS

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; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-09-423-233-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus S TITLE OF INVENTION: Other Filamentous Fung1
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09423233
Patent No. 6372430
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Local Similarity 100.0%;
les 310; Conservative 0
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CTGAACTTAA
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Pred. No. 2e-160;
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US-08-652-127C-7
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APPLICANT: Lee, May
APPLICANT: Lee, May
APPLICANT: Galazzo, Jorge
APPLICANT: Galazzo, Jorge
TITLE GALAZZO, Jorge
Production of High Titers of Gibberellins GA4 and GA7
FILE REFERENCE: L02-01NP
CURRENT APPLICATION NUMBER: US/09/645,073
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US/09/645,770
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08652127C Patent No. 5792611
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LENGTH: 2293
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Best Local Similarity
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ORGANISM: Gibberella fujikuroi
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Richard TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                   SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                     ATTORNEY/AGENT INFORMATION:
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STREET: bu.
STREET: Cana
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                                                                           APPLICATION NUMBER: US/08/652,127C FILING DATE: May 23, 1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                     COUNTRY: Canada ZIP: K1R 6K7
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 18
                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                             880 Wellington Street, Suite 708
                                                                                                                                                                                                                                                                                                                                                                                                       Richard C. Hamelin
VENTION: DETECTION OF PLANT
VENTION: PATHOGEN FUNGI
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Seaby & MacLean
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Pred. No. 1.2e-117;
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                                                                                                                                                           US-08-652-127C-6
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                                                                                             Matches
                                                                                                          Query Match
Best Local Similarity
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Best Local Similarity
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TELEPAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 18:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: May 23, 1:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DETECTION OF PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: doubl
TOPOLOGY: linear
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 880 | CITY: Ottawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby & MacLean
STREET: 880 Wellington Street, Suite 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                        LENGTH: 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCGCCAGTATTCTGGCGGGCA 87
                                                            28 AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCGGCCAGTATTCTGGCGGGCA 87
 88 TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCCCCGGG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K1R 6K7
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                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Richard C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                          May 23, 1996
                                                                                                                                                                                          double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.9%;
                                                                                                            100.0%;
                                                                                                            31.9%; Score 99; DB 1; Length 581 100.0%; Pred. No. 1e-44;
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Pred. No. 1e-44;
                                                                                             Mismatches
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                                                                                             Gaps
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US-08-887-480-82
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US-08-887-480-82
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ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
CTEANTENEES: 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 82, Applicat
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck,
                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
INDIVIDUAL ISOLATE: (consensus sequence)
FEATURE:
                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                           NAME/KEY: misc feature LOCATION: 13..161
OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature LOCATION: 1..12 OTHER INFORMATION: /note OTHER INFORMATION: rRNA
               OTHER INFORMATION:
                                                   NAME/KEY: misc_feature
LOCATION: 473..504
                                                                                                           OTHER INFORMATION:
                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                                                    NAME/KEY: misc feature LOCATION: 162..318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Tarrytown
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                                                                                                                             misc_feature
319..472
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                                                                                                           /note=
                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                  /note=
           /note= "5' end of large subunit
rRNA gene"
                                                                                                                                                                                                                                                                                                                                   /note= "3' end of small subunit
rRNA gene"
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                                                                                                                                                                                "5.8S rRNA gene"
                                                                                                           "ITS 2"
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RESULT 6
US-08-905-314A-19
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Best Local Similarity
Matches 94; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/08905314A Patent No. 5827695
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (919) 541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                              PEATURE:

NAME/KEY: misc feature
LOCATION: 1..12

OTHER INFORMATION: /note=
OTHER INFORMATION: rRNA g
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Beck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIE: 20779-2257

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                  FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (919) 541-8587
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                 LOCATION: 162.31
                                                                                                                NAME/KEY: misc feature LOCATION: 13..161
OTHER INFORMATION: /no
                                                                                                                                                                                                                                                                   ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
INDIVIDUAL ISOLATE: (consensus sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3054 commune CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/905,314A FILING DATE:
                 NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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                                                                 misc feature
162.318
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misc_feature
319..472
                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                         single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DETECTION OF WHEAT FUNGAL PATHOGENS USING THE POLYMERASE CHAIN REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.3%; Score 94; DB 1; L
100.0%; Pred. No. 5.8e-42;
                                                                                                                                                                                    rRNA gene"
                                                   /note=
                                                                                                                  /note=
                                                                                                                                                                                                       /note= "3' end of small subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38,241
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US-08-722-187-82
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Patent No. 5955274
GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

PRIOR APPLICATION UNMBER: US 08/233,608
APPLICATION NUMBER: US 08/233,608
APPLICATION NUMBER: US 08/233,608
APPLICATION INFORMATION:

NAME: Walsh, Andrea C.

REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Detection of Fungal Pathogens Using the TITLE OF INVENTION: Polymerase Chain Reaction NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ligon, James N
APPLICANT: Beck, James J
                                                                                                                 AYPOTHETICAL: NO
                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
               LOCATION: 1..504
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                 NAME/KEY: misc_feature
LOCATION: 1..504
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                LENGTH: 504 base pairs
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94; Conservative 0;
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473..504
                                                                                                                                                  linear
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                                                                                                                                   DNA (genomic)
                                                                                                                                                              single
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                               /note= "DNA sequence internal transcribed
                 (fculm.con)"
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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5.8e-42;
                                for the spacer region of Fusarium culmorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 504;
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US-09-481-293-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 82, Application PC/TUS9504712 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32, Application US/09481293 Patent No. 6485907
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Beck, James
APPLICANT: Barnett, Jason
APPLICANT: Barnett, Jason
TITLE OF INVENTION: PCR-Based Detection of Rhizoctonia cerealis
FILE REFERENCE: PB/5-31135P1
CURRENT APPLICATION NUMBER: US/09/481,293
CURRENT FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Fusarium culmorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 504
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Detection of Fungal Pathogens Using the TITLE OF INVENTION: Polymerase Chain Reaction NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ligon, James M
APPLICANT: Beck, James J
                                                                                                                                                                                                                              STREET: / CONTROL Hawthorne
                                                  CLASSIFICATION:
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                             ADDRESSEE: Clba-vc-2, coments; 7 Skyline Drive
                                                                                  APPLICATION NUMBER:
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Conservative 0;
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100.0%; Pred. No. 5.8e-42;
tive 0; Mismatches 0;
                                                                                  PCT/US95/04712
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8668
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 84, Application Patent No. 5814453
GENERAL INFORMATION:
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                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME/KEY: misc feature

LOCATION: 1..504

OTHER INFORMATION: /note

OTHER INFORMATION: inter

OTHER INFORMATION: (fcul
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Beck, James J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 520 White CITY: Tarrytown
                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08887480
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                                                                                                                                                                                                                                                                                                                         Floppy disk
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "DNA sequence for the
internal transcribed spacer region of Fusarium culmorum
(fculm.con)"
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RESULT 11
US-08-905-314A-21
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/08905314A Patent No. 5827695
                                             COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
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APPLICANT: Beck,
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ORIGINAL SOURCE:
ORGANISM: Fus
                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
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ATTORNEY/AGENT INFORMATION:
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IMMEDIATE SOURCE:
CLONE: pCRFMON1
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OTHER INFORMATION: /note OTHER INFORMATION: rRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: 336..488 OTHER INFORMATION: /no
              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                         ADDRESSEE: No. 5827695artis Corporation Patent Department STREET: 3054 Cornwallis Road CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                             STATE:
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LOCATION: 179..335
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LOCATION: 31..178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "5' end of large subunit
rRNA gene"
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rRNA gene"
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                                                                                                                                       3-08-887-480-96
Sequence 96, Application US/08887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the TITLE OF INVENTION: Polymerase Chain Reaction
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8887
TELEFAX: (919) 541-8689
                                                                                          NUMBER OF SEQUENCES: 96
CORRESSONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 545 base pairs
TYPE: nucleic acid
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                            STREET: 520
CTTY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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LOCATION: 489.545
OTHER INFORMATION: /note
OTHER INFORMATION: rRNA
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LOCATION:
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OTHER INFORMATION:
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LOCATION: 31..178
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                                                                                                                                                                                                                                                                                                                                                                                   94;
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                                               USA
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179..335
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rRNA gene"
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RESULT 13
US-08-905-314A-22
; Sequence 22, Application US/08905314A
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SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
ORIGINAL SOURCE:
                                                                                                                                                                                                                              Matches
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Best Local (
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IMMEDIATE SOURCE:
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FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                              LOCATION: 490..546
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 338..489
OTHER INFORMATION:
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LOCATION: 181..337
OTHER INFORMATION: /not
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OTHER INFORMATION:
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OTHER INFORMATION: rRNA gene"
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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                                                                                                  318
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pCRFpoaeT756(3-1)
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100.0%; Pred. No.
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GENERAL INFORMATION:

APPLICANT: Beck,

James J.

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                                                            Matches
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INFORMATION FOR SEQ ID NO:
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                                                                                LOCATION: 490..546
OTHER INFORMATION: /note= "5'
OTHER INFORMATION: rRNA gene"
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OTHER INFORMATION: /note
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LOCATION: 338..489
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INDIVIDUAL ISOLATE: T-427, T-534,
INDIVIDUAL ISOLATE: sequence)
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pCRFpoaeT756(3-1)
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3054 Cornwallis Road
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181..337
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31..180
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rRNA gene"
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Pred. No.
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                                                            Mismatches
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5. 7e-42;
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RESULT 15
US-09-423-233-6
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US-08-652-127C-5
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                           Sequence 6, Application US/09423233

Retent No. 6372430

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America as TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus STITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341WP

CURRENT APPLICATION UNMBER: US/09/423,233

CURRENT FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Patent No. 57
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
PILING DATE: MAY 23, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (613) 232-5831 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GEOTGE A. Seaby
REGISTRATION NUMBER: 24,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
NUMBER OF SEQUENCES: 10
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STRANDEDNESS: doub
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Seaby & MacLean
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Pred. No.
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; TYPE: DNA
; ORGANISM: Fusarium solani
US-09-423-233-6

Query Match
Pest Local Similarity 100.0%; Pred. No. 9.7e-34;
Best Local Similarity 100.0%; Pred. No. 9.7e-34;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Indels 0; Indels 0; Indels
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Perfect score:
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: /cgn2_6/ptodata/1/pubpna/USO7 NEW PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/PCTUS PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/PCTUS PUBCOMB.seq:*
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: /cgn2_6/ptodata/1/pubpna/USO9 PUBCOMB.seq:*
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0 US-09-961-755A-5

0 US-09-961-755A-5

0 US-09-961-755A-5

0 US-10-046-955-26

US-10-046-955-27

US-10-046-955-26

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0 US-09-961-663-15

0 US-09-961-663-16
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Sequence 5, Appli
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Sequence 6, Appli
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Sequence 27, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 11, Appl
Sequence 11, Appl
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Sequence 8721, Ap Sequence 3, Appli Sequence 59, Appl	28, Ap 4, App 2, App 3, App 1, App 57854,	360, 355, 25, 11, 7	Sequence 24, Appl Sequence 4, Appli Sequence 5, Appli Sequence 2, Appli Sequence 29, Appl	2, 1, 372 72,	18, 4, 4, 1, 1,

ALIGNMENTS

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APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 1908-05-01
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-10-046-955-7
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Publication No. US20030129600A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dist APPLICANT: Morrison, Christine J.
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Matches
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LENGTH: 310
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; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7
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APPLICANT: Barnett, Jason
APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
TITLE OF INVENTION: Detection Reaction
FILE REFERENCE: 60055
CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
     Sequence 6, Application US/09961755A Publication No. US20030113722A1 GENERAL INFORMATION:
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Sequence 8, Application US/09961755A

Publication No. US20030113722A1

GENERAL INFORMATION:
APPLICANT: Beck, Jim
APPLICANT: Barnett, Jason
TITILE OF INVENTION: Detection of Fusarium Species inf
TITILE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 60055
CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
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US-09-961-755A-8

infecting

Corn Using

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Sequence 5, Application US/09961755A

Publication No. US20030113722A1

GENERAL INFORMATION:
APPLICANT: Back, Jim
APPLICANT: Beck, Jim
FILE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 60055
CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT PRILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGUTH: 525
LINGUTH: 525
TYPE: DNA
ORGANIEM: Fisarium subglutinans
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CURRENT APPLICATION NUMBER: US/09/961,755A

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn version 3.0

SEQ ID NO 6

SEQ ID NO 6

LENGTH: 521

TYPE: DNA

ORGANISM: Gibberella zeae

US-09-961-755A-6
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Best Local S
Matches 94
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Best Local Similarity
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APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using
TITLE OF INVENTION: Polymerase Chain Reaction
                                                   316
                                                                                                                       316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCGCCAGTATTCTGGCGGGCA
                                                                                    88
                                                                                                                                             88 TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC 121
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                                                                                                                                                                                           94;
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                                                                                                                                                                                                            Similarity
                                                                                 TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC 121
                                                   TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC 349
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                                                                                                                                                                                           30.3%; Score 94; DB 10; ilarity 100.0%; Pred. No. 5e-43; Conservative 0; Mismatches 0
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5e-43;
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RESULT 7
US-10-046-955-27
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US-10-046-955-6
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                                               Sequence 27, Application US/10046955 Publication No. US20030129600A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 6
LENGTH: 319
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LENGTH: 522
TYPE: DNA
ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
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Best Local !
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APPLICANT:
APPLICANT:
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APPLICANT: The Government of the United APPLICANT: Secretary of the Department APPLICANT: Control and Prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR TILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Aidorevich, Liliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
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                                                                                                                                                                      TGCCTGTTCGAGCGTCATT 108
                                                                                                                                                                                                                                                                      TGCCTGTTCGAGCGTCATTTCAACCCTCAAGCCC 121
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Reiss, Errol
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100.0%; Pred. No.
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                 States of of Health
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5e-43;
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              America, as Represented by the and Human Services, Centers for
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APPLICANT: Choi, Jong Soo
ITILE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
ITILE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT PILLING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILLING DATE: 2000-06-27
PRIOR FILLING DATE: 1998-05-01
PRIOR FILLING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILLING DATE: 1998-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
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; ORGANISM: Scedosporium apiospermum
US-10-046-955-27
                                                                                                                                                               ; ORGANISM: Scedosporium apiospermum US-10-046-955-26
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US-10-046-955-26
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TITLE OF INVENTION: Nucleic Acids for Detecting Asj
TITLE OF INVENTION: Nucleic Acids for Detecting Asj
TITLE OF INVENTION: Other Filamentous Fungi
FILE REPERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
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Publication No. US20030129600A1
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APPLICANT: Morrison, Christine J.
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                                       AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCG 69
  AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCG
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                                                                                Conservative
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                                                                            Score 42; DB; Pred. No. 2.6
0; Mismatches
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                                                                                                                   Length 344;
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RESULT 10
US-09-961-663-15
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Patent No. US20020115084A1
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. :
SEQ ID NO 15
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APPLICANT: Barnett, Jason
APPLICANT: Beck, James
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LENGTH: 377
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                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Detection of Mycosphaerella TITLE OF INVENTION: Reaction FILE REFERENCE: PB/5-31382A CURRENT APPLICATION NUMBER: US/09/961,663 CURRENT FILING DATE: 2001-09-24 PRIOR APPLICATION NUMBER: US 60/211902 PRIOR FILING DATE: 2000-06-16
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                                                                                                                                                                      PRATURE:

PRATURE:

PRATURE:

PRAME/KEY: misc feature

NAME/KEY: misc feature

LOCATION: (1) (377)

OTHER INFORMATION: Truncated DNA sequence for the Internal

OTHER INFORMATION: Transcribed Spacer of fungus amplified from banana

OTHER INFORMATION: sample "Matouba bas 3"
                                                                                                                                                                                                                                                                                                LENGTH: 377
TYPE: DNA
ORGANISM: Mycosphaerella sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Truncated DNA sequence for the Internal OTHER INFORMATION: Transcribed Spacer of a fungus amplified from OTHER INFORMATION: banana sample "Capesterre-babin 2".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Mycosphaerella sp.
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LOCATION: (1)..(377)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
  118 AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCC 158
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                            28 AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCC 68
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; LOCATION: (1). (377)
; OTHER INFORMATION: Truncated DNA sequence for the Internal; OTHER INFORMATION: Transcribed Spacer of a fungus amplified from ; OTHER INFORMATION: banana sample "Temoin Infest Forte" US-09-961-663-16
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Best Local Similarity
Matches 41; Conserv
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CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/961,663
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain TITLE OF INVENTION: Reaction FILE REFERENCE: PB/5-31382A
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                                                                                                                                                                   TENGTH: 377

TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Consensus
OTHER INFORMATION: sequence of Mycosphaerella sp. ITS sequences shown
OTHER INFORMATION: in SEQ ID NO:14-16.
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Pred. No.
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Pred. No.
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9.7e-13;
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US-10-356-320-1

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RESULT 15
US-09-961-663-18
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; ORGANISM: Mycosphaerella fijiensis
US-09-961-663-17
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US-09-961-663-17
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APPLICANT: Beck, James
APPLICANT: Beck, James
TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
TITLE OF INVENTION: Reaction
FILE REFERENCE: PB/5-31382A
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US/09/961,663
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 534
Sequence 18, Application US/09961663
Patent No. US20020115084A1
GENERAL INFORMATION:
APPLICANT: Barnett, Jason
APPLICANT: Beck, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Strobel, Gary
APPLICANT: Ford, Eugene
APPLICANT: James, Harper K.

TITLE OF INVENTION: Pestalotiopsis Microsporia Isolates and Compounds Derived
TITLE OF INVENTION: Therefrom
FILE REFERENCE: A-72093 (470425-4)
CURRENT APPLICATION NUMBER: US/10/356,320
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/352,254
PRIOR APPLICATION NUMBER: US 60/352,254
PRIOR FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09961663 Patent No. US20020115084A1 GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pred. No.
Matches 41; Conservative 0; Mismatci
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TYPE: DNA
ORGANISM: Pestalotiopsis sp. NG12-30
ORGANISM: Pestalotiopsis sp. NG12-30
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank Acc. No. US20040009573A1 AF377301
DATABASE ENTRY DATE: 2002-06-02
RELEVANT RESIDUES: (1)..(466)
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; TYPE: DNA
; ORGANISM: Mycosphaerella musicola
US-09-961-663-18
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                                                                              Matches
                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain TITLE OF INVENTION: Reaction FILE REFERENCE: PB/5-31382A CURRENT APPLICATION NUMBER: US/09/961,663 CURRENT FILING DATE: 2001-09-24 PRIOR APPLICATION NUMBER: US 60/211902 PRIOR APPLICATION UMBER: US 60/211902 PRIOR PILING DATE: 2000-06-16 NUMBER OF 5EQ ID NOS: 19
258 AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCC 298
                      28 AATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCC
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                                                                          13.2%; Score 41; nilarity 100.0%; Pred. No. Conservative 0; Mismatci
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Search completed: October 1, 2004, 11:22:42 Job time: 278.951 secs

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Z93178	Z30406	92332	S07B5	87471	91687	93103	49209	87461	2325	2385	2358	0416	2309	2565	5118	5193	6143	6138	6106	6100	5682	5685	3460	5242	5006	7446	CB903866	4472	7029	5228	5148	5101	5213	5139	5197	5102	5200	5128	0703	9800	
Z931784	304060	Z923320	437434	874719	16873	31033	92096	74616	23253	23857	23588	04161	3094	25653	51183	51934	61430	61387	61064	61006	56827	56856	34605	52420	50064	74466	CB903866	44721	70292	52289	51484	51015	52136	51399	51971	51027	52001	51285	07036	00860	
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ALIGNMENTS

	JOURNAL COMMENT	TITLE	AUTHORS		SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION	RESULT 1 CF880267 LOCUS DEFINITION
Fungal Genomics Laboratory North Carolina State University Campus Box 7251, Raleigh, NC 27695, USA Tel: 919-513-0020 Fax: 919-513-0024 Email: ralph_dean@ncsu.edu Seq primer: LT-F1 primer.	Trichoderma reesei EST dataset Unpublished (2003) Contact: Ralph A. Dean	MICCRELL, T.K., van Solingen, P., Teunissen, P.J.M., ward, M. and Dean, R.A. Analysis of the protein processing and secretion pathways in a	Diener S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.	Hypocrea jecorina (anamorph: Trichoderma reesei) Hypocrea jecorina	CF880267.1 GI:38134949 EST.	Hypocrea jecorina cDNA clone tric081xc18, mRNA sequence. CF880267	CF880267 735 bp mRNA linear EST 31-OCT-2003 tric081xc18.b2 T.reesei mycelial culture, Version 6 October 2003

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JOURNAL COMMENT
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North Carolina State University
Campus Box 7251, Raleigh, NC 27695,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Hypocrea jecorina
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

(bases 1 to 739)
Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,
Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                Trichoderma reesei EST dataset
Unpublished (2003)
Contact: Ralph A. Dean
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primer: LT-F1 primer.
Location/Qualifiers
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       21.6%; Solitarity 100.0%; I Conservative 0;
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                                                                                           /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
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culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
                                                                                                                                                             /organism="Hypocrea
/mol_type="mRNA"
/strain="QM6a"
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/clone="tric081xc18"
/dev_stage="mycelia"
/dev_lib="T.reesei mycelial culture, Version 6 October
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/mol_type="mRNA"
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       Score 67; DB; Pred. No. 1.8
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Version 6 October 2003
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796 bp mRNA line tric024xb14 T.reesei mycelial culture, Version jecorina cDNA clone tric024xb14, mRNA sequence. CB900742 CB900742.1 GI:30115400 EST.
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomyco

Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (bases 1 to 755)

Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,

Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M.
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Hypocrea jecorina cDNA clone tricO24xj04, mRNA sequence.
CF870665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ralph_dean@ncsu.edu
Seq primer: LT-F1 primer.
Location/Qualifiers
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Unpublished (2003)
Contact: Ralph A. Dean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            North Carolina State University Campus Box 7251, Raleigh, NC 27-Tel: 919-513-0020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dean, R.A.
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llarity 100.0%;
Conservative
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/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
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/mol_type="mRNA"
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Version 6 October 2003
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925 Page Mill Road, 1
7el: (650) 846-7635
Fax: (650) 621-7817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67;
                                                                              Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S., Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J., Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C., Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M. Transcriptional regulation of biomass degrading enzymes in the filamentous fungus Trichoderma reesei J. Biol. Chem. 278 (34), 31988-31997 (2003)
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Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo A
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Hypocrea jecorina
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Location/Qualifiers
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/mol_type="mRNA"
/strain="QM6a"
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clone="tric024xb14"
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tive 0;
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CA 94304, USA
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Local Similarity hes 67; Conserv
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Genencor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 840)
1 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                we will be well tricostroid tricostroid T.reesei mycelial culture, Version jecorina cDNA clone tricostroid, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypocrea jecorina (anamorph: Hypocrea jecorina
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925 Page Mill Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997
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primer: LT-F1 primer.
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(650) 621-7817
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/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 3 april"
/clone="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
                                      /dev_stage="mycelia"
/clome_lib="T.reesei mycelial culture, Version 3 april"
/clome_lib="T.reesei mycelial culture, Version 3 april"
/note="Vector: pREBPY; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
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and Nitrogen
                                                                                                                                                                                                                                                                                                                      organism="Hypocrea/mol_type="mRNA"
                                                                                                                                                                                                            clone="tric081xc18"
                                                                                                                                                                                                                                                  db_xref="taxon:51453"
                                                                                                                                                                                                                                                                                         strain="QM6a"
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|mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foreman
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Pred. No. 1.8e-2
sources and
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England,G.J.,
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Best Local (
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Best Local Similarity
   Matches
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Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford C:
Tel: 612 625 1243
Fax: 651 649 5058
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BQ751285
l Similarity
45; Conserv
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ESTs from mycelia of Colletotrichum trifolii race 1
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: (gtA AtA CgA CtC ACt AtA ggg Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST631848 DSCT Colletotrichum trifolii cDNA clone pDSCT4-17, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAD17TV More
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colletotrichum trifolii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .medicago.org
   Conservative
                                                                                                                                                         /tissue type="mycelia"
/tissue type="mycelia"
/dev stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab host="DH5alpha"
/clone lib="DSCT"
/c
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                                                                                                                                                   recombinants.
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/clone="pDSCT4-17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain="race 1"
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100.0%; F
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100.0%; Pred. No.
14.5%; Score 45; DB
100.0%; Pred. No. 1e
ive 0; Mismatches
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. 1.8e-24;
                        DB 13; Length 704;
le-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAI22TV More information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_ESTs: EST632563
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ESTs from mycelia of Colletotrichum trifolii race 1
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Samac, D.A., Dickman, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 612 625 1243
Fax: 651 649 5058
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                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                   /clone lib="DSCT"
/clone lib="DSCT"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Solate: 2sp2; cDNA was prepared from polyA+
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
recombinants."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab_host="DH5alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="race 1"
/db_xref="taxon:5466"
/clone="pDSCT9-22"
/tissue_type="mycelia"
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/mol_type="mRNA"
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Pred. No. 1e-12;
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pDSCT9-22, mRNA
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DEFINITION

BQ751027 743 bp mRNA linear EST 18-JUL-2002 EST631590 DSCT Colletotrichum trifolii cDNA clone pDSCT2-20, mRNA

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RESULT 10
BQ751971
LOCUS
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BQ751027
BQ751027.1
                                                                                                                                     sequence.
BQ751971
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.
                                                           Colletotrichum trifolii
Colletotrichum trifolii
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EST632534 DSCT Colletotrichum
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Contact: Deborah A. Samac
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
University of Minnesota
Maps Borlaug Hall, 1991 Upper Buford
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Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utte Cheung, F. and Fraser, C.M.
ESTs from mycelia of Colletotrichum trifolii race 1
                                                                                                                   BQ751971.1 GI:21907376
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Colletotrichum trifolii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAB20TV More information
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                           ATTCTGGCGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGC 86
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/lab host="UH5alpha"

/clone_lib="DSCT"
/clone_lib="DSCT"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: EcoRI; isolate: 2sp2 ; cDNA was prepared from polyA+enriched RNA The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of
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Location/Qualifiers
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clone="pDSCT2-20"
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Borlaug Hall,
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                  Samac,D.A., Dickman,M., Town,C.D., Var
Cheung,F. and Fraser,C.M.
ESTs from mycelia of Colletotrichum tr
Unpublished (2002)
Other ESTs: EST631961
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
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Contact: Deborah A. Samac
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Cd
Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                      B0751399
B0751399.1 GI:21906804
EST.
Colletotrichum trifolii
Colletotrichum trifolii
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Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Ut Cheung,F. and Fraser,C.M.
ESTs from mycelia of Colletotrichum trifolii race
                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.

1 (bases 1 to 758)
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EST631962 DSCT Colletotrichum
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TIGR sequence name: MTSAIO3TV More
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/clone lib="DSCT"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
recombinants."
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/lab_host="DH5alpha"
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/clone="pDSCT9-3"
/tissue_type="mycelia"
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1991 Upper Buford Circle,
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trifolii cDNA clone pDSCT4-95, mRNA
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  St. Paul, MN 55108, USA
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RESULT 12
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Best Local Similarity
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                                                                                                                              Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle,
Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                                                                                                                  Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
ESTs from mycelia of Colletotrichum trifolii race 1
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.
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                                                                                          Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAJ23TV More information
                                                                                                                                                                                                                                                Other_ESTs: EST632698
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TIGR sequence name: MTSAD95TV More information is available at:
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Colletotrichum trifolii
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Fax: 651 649 5058
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organism="Colletotrichum trifolii"/
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/strain="race 1"
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Pred. No. 1e-12;
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Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper
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Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utto Cheung,F. and Fraser,C.M.
ESTs from mycelia of Colletotrichum trifolii race 1
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BQ751015.1 GI:21906420
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Fax: 651 649 5058
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TIGR sequence name: MTSAB07TV More information
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/tissue_type="mycelia"
/dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab_host="pHSalpha"
/clone_lib="DSCT"
/clone_lib="DSCT"
/clone_lib="DSCT"
/clone_Tyector: pBluescript SK+; Site_1: EcoRI; Site_2:
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
Iysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DHSalpha which
were plated onto medium with X-gal for selection of
/dev_stage="Young, actively growing mycelia (3 days after
inoculation) grown in liquid culture (cutin minimal medium
containing 2*glucose)."
/lab_host="DH5alpha"
                                                                                          tissue_type="mycelia"
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/strain="race 1"
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DSCT Colletotrichum ti
                                                                                                                'clone="pDSCT2-7"
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trifolii cDNA clone pDSCT2-7, mRNA
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Seq primer: (gtA AtA CgA CtC
Location/Qualifiers
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Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utte
Cheung,F. and Fraser,C.M.
ESTs from mycelia of Colletotrichum trifolii race 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
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EST632047 DSCT Colletotrichum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAB48TV More information is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 Borlaug Hall, 1991 Upper Buford Circle,
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Sordariomycetes incertae sedis; Phyllachorales
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Conservative (
                    /tissue type="mycelia"
/tissue type="mycelia"
/dev_stage="Young, actively growing mycelia (3 days after
inoculation) grown in liquid culture (cutin minimal medium
containing 2%glucose)."
/lab_host="DH5alpha"
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/clone lib="DSCT"
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/clone lib="DSCT"
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/clone lib="DSCT"
/state="wector: pBluescript SK+; Site_1: EcoRI; Site_2:
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gt11 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
ligate. The cDNA inserts were gel purified after EcoRI
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clone="pDSCT5-48"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       mol_type="mRNA"
strain="race 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Colletotrichum trifolii"
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trifolii cDNA clone pDSCT5-48, mRNA
into pBluescript SK+. Aliquots of
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JOURNAL COMMENT

TITLE

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FEATURES

source

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Matches Query Match

Local Similarity hes 45; Conserv

Conservative

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Mismatches

Indels

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ORGANISM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle,
Tel: 612 635 1243
Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAKSOTV More informati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utt. Cheung, F. and Fraser, C.M.
ESTs from mycella of Colletotrichum trifolii race 1
Unpublished (2002)
Other_ESTs: EST632851
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/clone lib="DSCT"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
recombinants."
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/dev stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2*glucose)."
/lab_host="DH5alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                /strain="race 1"
/db_xref="taxon:5466"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c: (gtA AtA CgA CtC ACt AtA cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          clone="pDSCT11-50"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Colletotrichum trifolii"
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Title: Perfect score:

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Scoring table: Sequence:

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3: gb_c

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AR206444
1 (bases 1 to 18)
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.So
Nucleic acids for detecting Aspergillus species and
filamentous fungi
Patent: US 6372430-A 50 16-APR-2002;
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PRISON, C.J., Reiss, E., Aidorevich, L. and Choi, J.S.
Norrison, C.J., Reiss, E., Aidorevich, L. and Choi, J.S.
Nucleic acids for detecting Aspergillus species and other
filamentous fungi
AL Patent: JP 2001525665-A 50 11-DEC-2001;
PHE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O
CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND
PREVENTION TECHNOLOGY TRANSFER OFFICE
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PN JP 200152565-A/50
PD 11-DEC-2001
PR 02-MAY-1998 JP 1998548275
PR 02-MAY
AP162898 335 bp DNA linear PLN 15-NOV-2001 Fusarium oxysporum f. sp. conglutinans 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

AP162898 AP162898.1 GI:5690387
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                                                                                                                                                                                                                                                                                            Direct Submission
Direct Submission
Submitted (28-JUN-1999) Biology, SangMyung
Submitted (28-JUN-1999) Biology, SangMyung
Submitted (28-JUN-1999) Biology, SangMyung
Submitted (28-JUN-1999) Biology, SangMyung
                                                                                                                                                                                                                                                                                                                                                                          Fusarium oxysporum f. sp. fragariae
Fusarium oxysporum f. sp. fragariae
Fusarium oxysporum f. sp. fragariae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium oxysporum complex.

1. (bases 1 to 335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP162899 335 bp DNA linear PLN 04-AUG-1999 Fusarium oxysporum f. sp. fragariae 5.85 ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 285 ribosomal RNA gene, partial sequence.

AP162899 AP162899
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Fusarium oxysporum f. sp. conglutinans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                              Min, B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF162899.1 GI:5690388
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Location/Qualifiers
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1 (bases 1 to 335)
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278. .>335
                                                                                       /product="internal
278. .>335
                                                                                                                                                                                   /db_xref="taxon:100903"
/note="forma specialis: fragariae
                                                                                                                                                                                                                       /organism="Fusarium oxysporum
/mol_type="genomic DNA"
/strain="MAFF 744009"
                                                                     /product="28S ribosomal RNA"
                                                                                                                       /product="5.8S ribosomal RNA"
|29. .277
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129. .277
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/mol_type="genomic DNA"
/strain="MAFF 744001"
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                                                                                                                                                                                                                                                                                                                                                                      163
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                                                                                                                                                                                                                                             AF339418 JAB DNA linear Fusarium oxysporum strain FS-1 5.8S ribosomal RNA sequence; internal transcribed spacer 2, complete ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                 1 CGTTAATTCGCGTTCCTC 18
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2 (bases 1 to 338)
Tooley, P.W., Hatziloukas, E.,
Direct Submission
Submitted (22-JAN-2001) Agric
                                                                                   Fusarium oxysporum complex.

1 (bases 1 to 338)

Tooley, P. W., Hatziloukas, E.,
Use of ligase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusarium oxysporum f. sp. raphani
Fusarium oxysporum f. sp. raphani
Fusarium oxysporum f. sp. raphani
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
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                                                                                                                                            Bukaryota; Fungi; Ascomycota; Pe
Hypocreomycetidae; Hypocreales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-JUN-1999) Biology, SangMyung Dong, Chong Ro-Gu, Secul 110-743, Korea
                                                        Unpublished
                                                                       infestans in potatoes
                                                                                                                                                                         Fusarium oxysporum
                                                                                                                                                                                         Fusarium oxysporum
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275. .>336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Fusarium oxysporum/mol_type="genomic DNA"/db_xref="taxon:96318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="28S ribosomal RNA"
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l29. .274
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orma_specialis: raphani"
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Pred. No. 24;
Agricultural Research Service, U.S.
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                            Scott, D.L.
                                                                                      for detection
                                                                                                                                             Pezizomycotina; Sordariomycetes; s; mitosporic Hypocreales; Fusarium;
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                            Carras, M.M.
                                                                                                                                                                                                                                                                             gene, partial
                                                                                                                                                                                                                                                              sequence; and 28S
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309
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                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 426)
Wang, Y. Y., Whitehead, M., Zhu, Y., Burns, A.,
Finsarium oxysporum f. sp. vanillae isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
AY383320
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Wang, Y.Y., Whitehead, M.,
Direct Submission
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Pusarium oxysporum f. sp. vanillae
Rusarium oxysporum f. sp. vanillae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY383320 426 bp DNA linear PNN 05-OCT-2 Fusarium oxysporum f. sp. vanillae isolate DL-1-1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGTTAATTCGCGTTCCTC 18
                                                                                                                                                                                                                                                                                                                                      University,
                                                                                                                                                                                                                                                                                                                                                 Submitted (08-SEP-2003) Dept.
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                                                                                                                                                                                                                                                                                                                                                                                                                            ITS 2 sequence
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                                                                         Similarity
                            CGTTAATTCGCGTTCCTC 18
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                                                       100.0%; ilarity 100.0%; Conservative 0
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spacer 2, and 28S ribosomal RNA"
                                                                                                                                                                                                                                          /organism="Fusarium oxysporum

'mol_type="genomic DNA"

/isolate="bL-1-1"

/db_xref="taxon:247126"
                                                                                                                                    product="internal transcribed"
                                                                                                                                                                product="5.8S ribosomal RNA"
                                                                                                                                                                                             product="internal transcribed
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/mol_type="genomic DNA"
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                                                                         Score 18;
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Pred. No. 24;
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                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                   Plant Pathology,
Kunming, Yunnan 6
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                                                          Indels
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650201, P
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P.R. China
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RESULT 8 AF502842/c

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SOURCE
ORGANISM
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DEFINITION
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AY387703
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AUTHORS
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Direct Submission
Submitted (10-SEP-2003) Department of Plant Pathology,
Plant Protection, Yunnan Agricultural University, Long
Kunming, Yunnan 650201, P. R. China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          441 bp DNA linear PLN 07-OCT-2
Fusarium oxysporum isolate DL-2-7 internal transcribed spacer 1,
partial sequence; 5.8S ribosomal RNA gene, complete sequence; an
internal transcribed spacer 2, partial sequence.
                                                                                                                                                                                                                              Fusarium oxysporum
Fusarium oxysporum
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreemycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 441)
                                                                                                               Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leaf litter ascomycete strain its331
leaf litter ascomycete strain its331
Eukaryota, Fungi, Ascomycota.
1 (bases 1 to 430)
Gilbert,G.S., Garbelotto,M., Chapela,I.,
                                                                                                                                               Unpublished
                                                                                                                                                              Fusarium oxysporum isolate DL-2-7 internal transcribed 5.8S ribosomal RNA gene and internal transcribed spacer
                                                                                                                                                                                                             Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-APR-2002) Environmental Studies, California, Santa Cruz, 1156 High St., Santa Ciccation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP502942 430 bp DNA linear PLN 13-MAY-2002 Leaf litter ascomycete strain its331 isolate 1000502849 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial
                                                                                                                                                                                                                                                                                                                                                           AY387703.1
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Gilbert, G.S., Garbelotto, M., Chapela, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biogeography of leaf litter fungi
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dreyfuss, M.M.
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                                                                                                                               (bases 1 to 441)
                                                                                                             Y.Y., Whitehead, M., Zhu, Y.Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="contains internal transcribed spacer 1, ribosomal RNA and internal transcribed spacer
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/specific_host="Miconia
/db_xref="taxon:194114"
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/strain="its331"
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/mol_type="genomic DNA"
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Pred. No. 24;
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                                                                                                           Burns, A.,
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                                                                                                           Hocking, T.,
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Tou Street,
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r 2 sequence
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2"
                                                                                                           Ruan, X.Y.
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AUTHORS
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                                                      Query Match
Best Local Similarity
Matches 18; Conserv
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JOURNAL
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 327
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                                                                                                                                                                                                                                                                                                                Submitted (03-SEP-2003) Plant Pathology, Yunnan Agricultural University, Longtou Street, Kunming, Yunnan 650201, Peoples Republic of China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusarium oxysporum f. sp. vanillae
Fusarium oxysporum f. sp. vanillae
Fusarium oxysporum f. sp. vanillae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

1 (Dases I to 445)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AY380575 445 bp DNA linear PLN 04-OCT-2003 Fusarium oxysporum f. sp. vanillae internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

AY380575 AY380575
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                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
2 (bases 1 to 445)
Wang, Y.Y., Whitehead, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGTTAATTCGCGTTCCTC 18
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                           CGTTAATTCGCGTTCCTC
                                                       Conservative
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                                                                                                                                                                                                                               /mol type="genomic DNA"
/isolate="HK-5a-4"
/db xref-"---
                                                                                                                                           /product="5.8S ribosomal RNA" 294. .>445
                                                                                                                                                                                    /product="internal transcribed spacer 1"
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                            product="internal transcribed"
                                                                                                                                                                                                             note="forma_specialis: vanillae"
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/mol_type="genomic DNA"
/isolate="DL-2-7"
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                                                                   Score 18; DB
Pred. No. 24;
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Pred. No.
                                                         Mismatches
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RESULT 12
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                                                                     Fusarium oxysporum f. sp. vanillae
Fusarium oxysporum f. sp. vanillae
Fusarium oxysporum f. sp. vanillae
Eukaryota; Fung;; Accomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari
Fusarium oxysporum complex.

1 (bases 1 to 445)
                                                                                                                                                                                                                                          AY387699 445 bp DNA linear PLN 07-OCT-2 Pusarium oxysporum f. sp. vanillae isolate DL-4b internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-SEP-2003) Department of Plant Protection, Yunnan Agricultural Kunming, Yunnan 650201, P. R. China Location/Qualifiers
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Fusarium oxysporum f. sp. vanillae
Fusarium oxysporum f. sp. vanillae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium oxysporum complex.

1 (bases 1 to 445)
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Fusarium oxysporum f. sp. vanillae isolate DL-4b internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
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Wang, Y.Y., Whitehead, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A.,
                                  and Liao, B.
                                                 Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y
                                                                                                                                                                                            AY387699.1 GI:37362904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular investigation of isolates of Fusarium oxysporum in relation to the control of root rot disease in vanilla planifolia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liao, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="5.8S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="internal transcribed
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mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="internal
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В
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University, Long
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Tou Street
                                                                                                         Fusarium;
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Direct Su
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                                                                                                                                                                                                            Submitted (10-SEP-2003) Department of Plant Pathology, Plant Protection, Yunnan Agricultural University, Long Kunming, Yunnan 650201, P. R. China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusarium oxysporum
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcribed spacer 2 sequence
Unpublished
2 (Dases 1 to 445)
Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T.,
                                                                                                                                                                                                                                                                                                                         Wang,Y.Y., Whitehead,M., Zhu,Y.Y.,
                                                                                                                                                                                                                                                                                                                                                                 5.8S ribosomal 
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                       Fusarium oxysporum isolate ML-7-1 internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang,
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ng,Y.Y., Whitehead,M., Zhu,Y.Y.,
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                                                                                                                                                    /organism="Fusarium oxysporum"
/mol_type="genomic nnn"
/product="internal
                                                                                                            db_xref="taxon:5507"
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136. .293
                                      'product="5.8S ribosomal RNA"
                                                                            product="internal transcribed"
                                                                                                                                    mol_type="genomic DNA"
isolate="ML-7-1"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                   spacer
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Tou Street
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AY387704
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KEYWORDS
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AY387705
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JOURNAL
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Best Local :
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Matches
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AY5 bp DNA linear PLN 07-OCT-200 Fusarium oxysporum isolate ML-8-4 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

AY387704
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18; Conserv
                                                                                                                  AY387705 AY387705 DNA linear PLN 07-OCT Fusarium oxysporum isolate ML-5-2 internal transcribed spacer partial sequence; 5.8S ribosomal RNA gene, complete sequence; internal transcribed spacer 2, partial sequence
                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China Location/Qualifiers
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1 (bases 1 to 445)
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                                                                                                       partial sequence; 5.8 internal transcribed AY387705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 445)
Wang, Y.Y., Whitehead, M., Zhu, Y.Y.,
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
                                 Fusarium oxysporum
                                                                                       AY387705.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y.
                                                   Fusarium oxysporum
                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                             CGTTAATTCGCGTTCCTC 344
                                                                                                                                                                                                                                                                                               CGTTAATTCGCGTTCCTC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 18; DB ilarity 100.0%; Pred. No. 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="5.8S ribosomal 294. .>445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:5507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mol_type="genomic DNA"
/isolate="ML-8-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Fusarium oxysporum"
                                                                                                                                                                                                                                                                                                                                                                                                                   product="internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="internal transcribed
                                                                                       GI:37362910
                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 293
                                                                                                                                                                                                                                                                                                                                 <u>,</u>
                                                                                                                                                                                                                                                                                                                                               Score 18;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                 red. No. 24;
Mismatches
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Search completed: October Job time: 148.108 secs

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2004, 05:17:02

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Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
Location/Qualifiers
1. .445
                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 445)
Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y.
and Chen, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Chen,J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusarium oxysporum isolate ML-5-2 internal transcribed spacer 1, 5.88 ribosomal RNA gene and internal transcribed spacer 2 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusarium oxysporum complex.
1 (bases 1 to 445)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to
                   CGTTAATTCGCGTTCCTC 18
CGTTAATTCGCGTTCCTC 344
                                                             Conservative
                                                                                                                                                                                                                              /db_xref="taxon:5507"
                                                                                                                                                                                                                                                /organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="ML-5-2"
                                                                                                                                      product="internal transcribed"
                                                                                                                                                                                               product="internal transcribed
                                                                                                                                                                     product="5.8S ribosomal RNA"
                                                                          100.0%;
                                                                                                                                                        . >445
                                                             0,
                                                                            Score 18;
Pred. No.
                                                             Mismatches
                                                                             24;
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Title:
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 2000000000
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1: geneseqn1980s:*
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3: geneseqn2000s:*
4: geneseqn2011as:*
5: geneseqn2011bs:*
6: geneseqn2002s:*
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10: geneseqn2004s:*
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18
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SUMMARIES

Result

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Abl12624 Drosophil Abl02050 Drosophil	Aas52883 Enterococ	Aca32983 Prokaryot	_	Abq28091 Oligonucl	Abl12625 Drosophil	Acf65787 Photorhab			Abq14482 Oligonucl	Adc92275 E. faeciu	Abs99066 Enterococ	Aax13271 Enterococ	Aca18462 Prokaryot	Acal2661 Prokaryot	Aas47978 Enterococ	Aas48419 Enterococ			Abq37055 Oligonucl	Aaa72783 5.8s rRNA	Aav83697 Species-s	Description

New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothrix

Example 1; Page 22; 45pp; English

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114 14	14.4 14.4	14.4 14.4	14.4 14.4	14.4 14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.8	14.8	14.8	14.8	14.8
77.8 77.8 77.8	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	82.2	82.2	82.2	82.2	82.2
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ABQ29382 ABQ29383 ABQ36596	ABQ69245_02 ABQ67197_01	AAD57212 AAD57200	AAH54455 ABL28982	AAH53833 ABN91904	ABQ34054	ABQ34055	ABQ18323	ABQ18322	ABK79312	ABZ26380	ACF65387_5	ACF67367_53	ABL02692	ACF72118	ABL03754
Abg29382 Oligonuci Abg29383 Oligonucl Abg36596 Oligonucl	44	Petunia 8.5 Kb	Aah54455 S. epider Abl28982 Drosophil	Aan53833 S. epider Abn91904 Staphyloc	_	Abq34055 Oligonucl	Abq18323 Oligonucl	Abq18322 Oligonucl	Abk79312 Bacillus	Abz26380 Candida e	Continuation (6 of	Continuation (54 o	Abl02692 Drosophil	Acf72118 Photorhab	Abl03754 Drosophil

ALIGNMENTS

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Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. funigatus; M. circinilloides f. circinelloides; R. fusopus oryzae; R. microsporus; R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum; Penicillium notatum; Sporothrix schenkii; filamentous fungus; ss.
                                                                                 WPI; 1999-034737/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV83697;
                                                                                                        Morrison CJ, Reiss E,
                                                                                                                                                       02-MAY-1997;
                                                                                                                                                                              01-MAY-1998;
                                                                                                                                                                                                      12-NOV-1998.
                                                                                                                                                                                                                              WO9850584-A2.
                                                                                                                                                                                                                                                                            modified_base
                                                                                                                                                                                                                                                                                                               Fusarium oxysporum.
                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species-specific probe targeted to the internal transcribed spacer 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV83697 standard; DNA; 18
                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                         97US-0045400P.
                                                                                                                                                                              98WO-US008926
                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/note= "labelled with digoxigenin"
                                                                                                          Aidorevich L, Choi JS;
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                          The invention relates to a nucleic acid based method for the detection of Alternaria contamination in a food product. The method involves obtaining and analysing a food product sample for a nucleic acid sequence unique to Alternaria. Detectable levels of the nucleic acid sequence can be used as an indication of Alternaria contamination. Fungi from the genus Alternaria are ubiquitous saprophytes and are economically important pathogens affecting a wide range of plants. Alternaria are the causative agents of black or brown spot disease in many fruits, vegetables and field crops. The method is used for the detection of Alternaria food products. The present sequence represents the pusarium oxysporum 5.8s rRNA gene, used in examples illustrating the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probes AAV83677-708 are derived from the internal transcribed spacer 2 (ITS2) region of various filamentous fungi (see AAV70845-73). The probes are species specific, and can be used for identifying a species selected from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans, F. starium solani, F. moniliforme, Mucor rouxi, M. racemosus, M. plumbeus, M. circinilloides f. circinelloides, Rhizopus oryzae, R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallesheria boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenkii. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi
                                                                                                                                                                                                                                                                       Nucleic acid based assay and kit for detection of Alternaria contamination in food products involves analyzing the sample product for nucleic acid sequences unique to Alternaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Black spot disease; brown spot disease; fungi; fruit vegetable; field crop; Alternaria; 5.8s rRNA; detection; ds.
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                                                                                                                                                                                                                                         Example; Fig 1; 47pp; English
                                                                                                                                                                                                                                                                                                                                               WPI; 2000-499381/44.
                                                                                                                                                                                                                                                                                                                                                                             Kashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JAN-2000; 2000WO-US001466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200046397-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusarium oxysporum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA72783 standard; DNA; 382 BP
                                                                                                                                                                                                                                                                                                                                                                                                                 (TECR ) TECHNION RES & DEV FOUND (KASH/) KASHI Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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Pred. No. 6.2;
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AC ABQ370
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AC ABQ370
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Oligon
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WHuman;
KW Human;
KW Gastro
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WO2002
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O1-SEP
PM 01-SEP
PM CLaim
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                                                 CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the CC degree of hybridisation to both classes is determined from the label on CC the amplicon. From the ratio of labels hybridised to the two classes of CC oligomers, the degree of methylation is calculated. The method is used: C1 if or diagnosis and/or prognosis of side effects of therapeutic drugs CC and of a wide range of diseases, e.g. cancer disorders of the central CC nervous, cardiovascular, gastrointestinal and respiratory systems etc., C particularly by detecting mutations or single nucleotide polymorphisms CC (SNP's); and (ii) for differentiation of cell or tissue types and for C investigating cell differentiation. The method allows the methylation CC status of many C residues to be determined simultaneously. ABQ13410-C2 ABQ54121 represent genomic DNA sequences used to illustrate the method CC disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention methylation of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis and prognosis,
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05-SEP-2000; 2000DE-01044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    describes a novel method for determining the degree of a particular cytosine in a motif 5'-CpG-3', present in
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Pred. No.
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                                                                                      This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, CC of oligonuclectides and/or peptide-nucleic acid (PNA) oligoners and the Cdegree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of CC oligoners, the degree of methylation is calculated. The method is used: (a) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central CC nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms CC (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation CC status of many C residues to be determined simultaneously. ABQ1310-CC ABQ54121 represent genomic DNA sequences used to illustrate the method CC disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12;
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05-SEP-2000;
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    l Similarity
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2000DE-01044543.
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0; Mismatches 1;
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                                                       CC the 6213 antitation for compression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense complete acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense compression is inhibited by the antisense complete acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation or the activity of gene or sellular proliferation or the biological pathway of the proliferation or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling the expressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the gene proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational contents of a compound that inhibits the
        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the 6213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or scrufor homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; ss; prokaryotic essential gene; cell proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolate candidate molecules for rational drug discovery programs
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Carr GJ,
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Forsyth
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Xu HH;
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The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the genes, CC their use in the discovery of novel antibiotics, the essential genes CC themselves and the encoded proteins. The prokaryotes used are Escherichia Coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, CC pseudomonas aeruginosa and Enterococcus faecalis. The invention is also CC useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify CC proteins used in proliferation, to express these proteins, and to obtain CC antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The cantisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense oligonucleotide of the invention. Note: The sequence data for this patent did not form part of
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26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001; 2001WO-US009180
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2000US-0257931P.
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Pred. No.
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                                     The invention relates to antisense inhibitors of genes essential to correct prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antisodies capable of binding to the expresses these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is also useful to screen for homologous invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibiotics,
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15; Conserv
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Xu HH;
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                    The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid CC encoding a polypeptide whose expression is inhibited by the antisense cc nucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the cativity of antisense nucleic acid; (4) an antibody capable of specifically binding CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for CC proliferation; (7) identifying a compound that influences the activity of dentifying a gene required for cellular proliferation or that has an activity against a biological pathway considered for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene CC compound's activity; (11) a culture comprising strains in which the gene constrains in
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

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antisense nucleic acids, useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation to late candidate molecules for rational drug discovery programs.

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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the 6213 antisense sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at
                                                                                                                                                                                                                  06-MAR-2002;
                                                                                                                                                                                                                                                                      21-MAR-2002; 2002WO-US009107
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Yamamoto R
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cc proliferation; (7) identifying a compound that influences the activity of ct the gene product or that has an activity against a biological pathway cc required for proliferation, or that inhibits cellular proliferation; (8) cidentifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies cor a gene on which the test compound that inhibits proliferation of an cc compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent cc which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the coroliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required cor proliferation to isolate candidate molecules for rational cc drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, cc prokaryotic essential genes. Note: The sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did cot form part of the printed specification, but was obtained in celectronic format directly from WIPO at cc fip. wipo.int/pub/published_pct_sequences
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16-MAY-1997;
14-NOV-1997;
     New isolated Enterococcus faecalis polynucleotides and polypeptides used to develop products for the detection of Enterococcus and for vaccines for prevention or attenuation of Enterococcus infection.
                                                                                                                            WPI; 1999-045171/04
                                                                                                                                                                                     Kunsch
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97US-0066009P.
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100.0%; Pred. No.
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Claim 1; Page 1436-1441; 2084pp; English.

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Enterococcus faccalis nucleotide sequence. The invention is useful to diagnose the presence of E.faecalis in a sample or determining the presence of a specific microbe in a sample. The invention is also useful for modulating the growth or pathogenicity of E.faecalis, in a vaccine to confer resistance to Enterococcal infection, for commercial, therapeutic and industrial purposes, and for fermenting a particular sugar source or to produce a particular metabolite. The invention is useful for detecting diseases related to Enterococcus infections in animals, and for detecting E.faecalis using biochip technology. The present nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KUNS/) KUNSCH (DILL/) DILLON 1 (BARA/) BARASH (
                                                                                                                                                                                                                                                                                                                                                nucleotide sequence useful for detecting infections in animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer readable medium; Enterococcus faecalis; microbe; growth; pathogenicity; vaccine; resistance; Enterococcal infection; commercial; therapeutic; industrial; fermanting; sugar source; metabolite; vaccine; biochip technology; antibacterial; modulator of nucleic acid expression
                                                                                                                                                                                                                                                                                                                   Claim 1; Page; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-750065/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecalis contig sequence #334.
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                                                                                                                                                                                                                                                          present invention relates to a new computer readable
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                                                                                                                                                                                                                                                                                                                                                                                                 on it a Enterococcus faecalis diseases related to Enterococ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2529 T;
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RESULT 12
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                       cc sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a cc recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. Cc The nucleic acids is useful for diagnosing pathological conditions cresulting from E. faecium bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans concleic acid is useful for recombinant production of Candida albicans and vaccines or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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ADC92275 standard; DNA; 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecium encoding an Enterococcus faecium polypeptide one of 10 fully defined sequences given in the (or comprising 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represents an Enterococcus faecalis contig DNA sequence of the invention.

Note: The sequence data for this patent did not form part of the printed specification but was obtained in Alactorian form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid derived from Enterococcus faecium encoding Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 1902; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-799836/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1997;
14-MAY-1998;
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abdominal-pelvic infection.
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98US-0085598P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9212;
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Query Match

Sequence

554 BP;

76 A; 67 C;

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242 T; 0 U; 0 Other;

Score 14.8;

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RESULT 13
ABQ14482
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Best Local
oligomers, the degree of methylation is calculated. The method is used:
(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation attains of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of the magnitude of the transfer of the sample of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 207 BP; 68 A; 36 C;
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gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; 56pp + Sequence Listing; 56pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons
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05-SEP-2000; 2000DE-01044543.
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Pred. No. 3.4e+02;
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RESULT 14
ABQ14483/c
                                                              This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one member, CC of oligonuclectides and/or peptide-nucleic acid (PNA) oligoners and the CC degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of CC oligoners, the degree of methylation is calculated. The method is used: CC in for diagnosis and/or prognosis of side effects of therapeutic drugs CC and of a wide range of diseases, e.g. cancer, disorders of the central CC nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms CC investigating cell differentiation. The method allows the methylation CC investigating cell differentiation. The method allows the methylation CC angostic of the degree of cytosine methylation described in the method of the degree of cytosine methylation described in the method colorers of the degree of cytosine methylation described in the
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gastrointestinal; respiratory system; single nucleotide polymorphi
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; 56pp + Sequence Listing; 56pp; German
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05-SEP-2000; 2000DE-01044543.
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0; Mismatches 2
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Search completed: October Job time: 37.9347 secs

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                                                                                                                                                                                                                                                                                                                                                                                             The sequences shown in AASO5401-AASO5661 represent DNA with mammalian vestibular system-modulating activity. The DNA sequences can be used in a method whereby a first and second strain of an invertebrate is obtained, and both are subjected to conditions in which the strains exhibit different geotactic behaviour. Genes that are differentially expressed in the first strain relative to the second strain are then identified. Mammalian genes having substantially the same nucleic acid sequence as these modulate the mammalian vestibular system. Compounds containing these genes are used to decrease the symptoms of graviperceptive
                                                                                                                                                                                                                                                                                                    disorders such as motion sickness, vertigo, labyrinthitis, Meniere's disease, acoustic neuroma, multiple sclerosis, syphilis, trauma, infection of the middle ear, exposure to ototoxic agents and epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalian vestibular system; invertebrate; geotactic behaviour; vert graviperceptive disorder; motion sickness; labyrinthitis; syphilis; Meniere's disease; acoustic neuroma; multiple sclerosis; epilepsy; trauma; infection of the middle ear; ototoxic agent exposure.
                                                                                                                                                                                                                                                Sequence 650 BP; 182 A; 181 C; 167 G; 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid having mammalian vestibular system-modulating activity useful in the treatment of disorders such as motion sickness and
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26-SEP-2000;
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                             US-09-423-233-50
US-09-134-000C-314
US-09-137-502A-1902
US-09-669-751-103
US-09-134-000C-2950
US-09-134-000C-2950
US-07-972-791-7
US-07-972-791-7
US-07-972-791-8
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US-09-277-700-1 US-09-874-585D-1	US-09-181-183-1 US-09-280-040-1	US-09-489-039A-11 US-09-489-039A-1305	US-09-561-741A-10 US-09-558-795-10	US-10-204-708-94 US-09-139-617-10	US-09-620-312D-176 US-09-185-501B-12	US-09-489-039A-409 US-09-833-381-1392	US-09-328-352-3243 US-09-134-000C-1003	US-09-453-702B-60 US-07-972-791-1
Sequence 1, Appli Sequence 1, Appli	Sequence 1, Appli Sequence 1, Appli	Sequence 11, Appl Sequence 1305, Ap	Sequence 10, Appl Sequence 10, Appl	Sequence 94, Appl Sequence 10, Appl	Sequence 176, App Sequence 12, Appl	Sequence 1392, App Sequence 1392, Ap	Sequence 3243, Ap Sequence 1003, Ap	Sequence 60, Appl Sequence 1, Appli

ALIGNMENTS

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; Sequence 50, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 50
LEBUOTH: 18
; TYPE: DNA
; ORGANISM: Fusarium oxysporum
US-09-423-233-50
                                                                                              APPLICANT: LYNI DOUGETTE-Stamm et al
APPLICANT: LYNI DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC:
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOI
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTMARE: PatentIn version 3.1
SEQ ID NO 314
LENGTH: 615
                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-09-134-000C-314
; Sequence 314, Application US/09134000C
; Patent No. 6617156
                                ; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1902:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...207
SEQUENCE DESCRIPTION: SEQ ID NO: 1902:
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                               Similarity
                                                                                                             CGTTAATTCGCGTTCCTC 18
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                                                                                CGTTAATTCTCTTTCCTC 67
                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (781)893-8277
Application US/09669751
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09107532A
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                                                                                                                                                               82.2%;
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                                                                                                                                                                 Score 14.8;
Pred. No. 4
                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                 44;
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                                                                                                                                                                               DB 4;
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                                                                                                                                                                               Length 207;
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 103
LENGTH: 650
TYPE: DNA
ORGANISM: Drosophila
US-09-669-751-103
                                                                                                                                                                                       US-09-134-001C-1367/c
Sequence 1367, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
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US-09-134-000C-2950/c
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
SEQ ID NO 2950
LENGTH: 2457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2950, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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APPLICANT: Greenspan, Ralph J.
APPLICANT: Greenspan, Ralph J.
TITLE OF INVENTION: Methods for Identifying Compounds for
TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related
TITLE OF INVENTION: Balance and the Perception of Gravity
FILE REFERENCE: P-NI 3864
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                           APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/669,751
CURRENT FILLING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/168,579
PRIOR FILING DATE: 1999-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                          963 CGTTAATTCCCGTTCCGC 946
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Pred. No. 54;
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Pred. No. 4
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RESULT 8
US-07-972-791-7/c
; Sequence 7, Application US/07972791
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US-07-972-791-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 93.8
15; Conservative
                                                                                                                                                  Matches
                                                                                                                                                                                Query Match
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SEQ ID NO 1367
                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3208 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 1921106
                                                                                                                                                                                                                            MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella abortus
STRAIN: biovar 1 (S2308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ficht, The APPLICANT: Sowa, Blai APPLICANT: Adams, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kettelberger, Denise M. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 963
                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 713-850-0165
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 713-
TELEX: 792026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 77027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1177 V
CITY: Houston
                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                 ocal Similarity 100.0%;
                                                                                    1488 GTTAATTCGCGTTC 1475
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                                                                                                                                                14; Conservative
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                                                                                                                  2 GTTAATTCGCGTTC 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: PRAVEL, GAMBRELL, HEWITT, & KRIEGER 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ficht, Thomas A. Sowa, Blair A.
                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                         single
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93.8%;
                                                                                                                                                               77.8%; Score 14; 100.0%; Pred. No.
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9: Pred. No. 82;
0; Mismatches
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TELEFAA:
TELEX: 792026
TILEX: 792026
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3345 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                              US-07-972-791-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; STRAIN:
US-07-972-791-7
                                                                                                                                                                                                                                      Sequence 5, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5348857
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: PRAVEL, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kettelberger, Denise M. TELECOMMUNICATION INFORMATION: TELEPHONE: 713-850-0909
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                     Local Similarity hes 14; Conserv
                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 713-850-0165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                     E: PRAVEL, GAMBRELL, HEWITT, & KRIEGER 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: PRAVEL, GAMBRELL, HEWITT, & KRIEGER 1177 West Loop South, 10th Floor
                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14; DB; Pred. No. 1.0
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hes 0;
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RESULT 10
US-07-972-791-2/c
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              INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3347 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application Patent No. 5348857
GENERAL INFORMATION:
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Matches 14; Conserva
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TELEX: 792026
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: KELTelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING TO THE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 3346 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 TELEFAX: /10
TELEFAX: 792026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1. TOTTY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
ORGANISM: Brucella abortus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: PRAVEL, GAMBRELL, HEWITT, & KRIEGER 1177 West Loop South, 10th Floor
                                                                                                                                                                                             713-850-0165
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RESULT 12 US-07-972-791-6/c

Sequence 6, Application US/07972791 Patent No. 5348857

GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.

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US-07-972-791-2
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                                                                Matches
                                                                                Query Match
Best Local Similarity
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APPLICANT: Ficht, Thomas A
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 3347 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
                                                                                                                                                                                 MOLECULE TYPE: O
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/972,791
FILING DATE: 19921106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
                                                                                                                                                ORGANISM: Brucel:
STRAIN: biovar 1
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TELEX: 792026
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TELEPHONE: 713-850-0165
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ZIP: 77027
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STATE: Texas
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1488 GTTAATTCGCGTTC 1475
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                               2 GTTAATTCGCGTTC 15
                                                                14; Conservative
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1177 West Loop South, 10th Floor
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                                                                                77.8%; Score 14; DB 1; 100.0%; Pred. No. 1.5e+(
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                                                                    Mismatches
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                                                                                 1.5e+02
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                                                                                                 Length 3347;
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RESULT 14
US-09-543-681A-4125/c
; Sequence 4125, Application US/09543681A
; Patent No. 6605709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Brucella ovis US-07-972-791-6
                                                                                                                                                                                                                                                                                                                   OF BRUCELLA
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                     SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3361 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                 Query Match
Best Local Similarity
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Best Local :
                                                                                                                                                                                  Matches
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FILING DATE: 1921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEPAX: 713-850-0165
                                                                                                                                                                                                                                                                                                                                                                                           ent No. 5310649

APPLICANT: Ficht, Thomas A.; Sowa, Blair A.; Adams, Garry L.
TITLE OF INVENTION: METHOD OF DETECTING SPECIES AND BIOVARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Adams, L. Gary
TITLE OF INVENTION: SPECIES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                        FILING DATE: 22-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 77027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                       LENGTH: 3434
                                                                                                            1692 GTTAATTCGCGTTC 1679
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.8%; Score 14; DB 1; Length 3361; larity 100.0%; Pred. No. 1.5e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                              77.8%; Score 14; DB 6; L
100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                Indels
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4125
LENGTH: 702
TYPE: DNA
ORGANISM: Proteus mirabilis
US-09-543-681A-4125
                                                                                                                   Query Match
Best Local Similarity
"~*~hes 15; Conserva
Search completed: October Job time: 7.93182 secs
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                                                                                                 5
                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1886
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US-09-328-352-1886
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                                                                                                                                                                                                                                                      APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1886
LENGTH: 1356
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1886, Application US/09328352 Patent No. 6562958 GENERAL INFORMATION:
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Pred. No. 1.8e+02;
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Maximum Match 100%
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Maximum DB
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seg length: 2000000000
Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

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19: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

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19: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Search time 73.304 Seconds (without alignments) 1244.847 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	ב	N	w	4.	u	n	7	8	9	10	11	12	13	14
Score	18	15.4	15	15	15	15	15	15	14.8	14.B	14.8	14.8	14.8	14.8
Query Match	100.0	85.6	83.3	83.3	83.3	83.3	83.3	83.3	82.2	82.2	82.2	82.2	82.2	82.2
Query Match Length DB	18	4461	127	128	250	250	1467	9212	262	438	585	650	3135	3138
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ID	US-10-046-955-50	US-10-437-963-93618	US-10-282-122A-978	US-09-815-242-996	US-09-815-242-555	US-10-282-122A-531	US-10-282-122A-6332	US-09-070-927A-334	US-09-535-459-1371	US-10-424-599-43896	US-10-437-963-81762	US-10-255-536-103	US-10-282-122A-20853	US-09-815-242-6520
Description	Sequence 50, Appl	Sequence 93618, A	Sequence 978, App	Sequence 996, App		Sequence 531, App	Sequence 6332, Ap	Sequence 334, App	Sequence 1371, Ap	Sequence 43896, A	Sequence 81762, A	Sequence 103, App	Sequence 20853, A	Seguence 6520. Ap

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13.8	13.8	13.8	13.8	13.8	14	14	14	14	14	14	14	14	14	14	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.8
76.7	76.7	76.7	76.7	76.7	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	80.0	0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	0	0	80.0	80.0	80.0	82.2
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US-09-987-899-169	US-09-987-899-160	US-09-987-899-182	US-10-424-599-93085	US-09-987-899-201	US-10-433-793-6	US-10-437-963-93655	US-10-369-493-36500	US-10-437-963-93584	US-10-437-963-93615	US-10-437-963-93471	US-10-437-963-93609	US-10-437-963-93652	US-10-424-599-59514	US-10-424-599-59512	US-10-398-221-2058	US-10-398-221-10	US-10-341-200-19	US-10-341-200-42	US-10-424-599-116221	US-10-424-599-78398	US-10-369-493-35000	US-10-027-632-266929	US-10-027-632-266929	US-10-029-386-7594	US-09-974-300-6603	US-10-242-535A-247	US-10-085-783A-247	US-10-032-585-259	US-10-297-465A-1
• •	Sequence 160, App	182,	9308		Sequence 6, Appli		Sequence 36500, A		93615,	Sequence 93471, A	93609,		Sequence 59514, A	Sequence 59512, A	N	e 1	19	Sequence 42, Appl	11				2669	Sequence 7594, Ap	5603,	-	247,	Sequence 259, App	Sequence 1, Appli

ALIGNMENTS

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SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 50
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Fusarium oxysporum
US-10-046-955-50
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Publication No. US20030129600A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dist APPLICANT: Control and Prevention

APPLICANT: Morrison, Christine J.

APPLICANT: Reiss, Errol

APPLICANT: Reiss, Errol
                                                                             Matches
                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                 APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR APPLICATION NUMBER: D5-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                             l Similarity
18; Conserv
CGTTAATTCGCGTTCCTC 18
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                                                                             100.0%; Score 18; DB llarity 100.0%; Pred. No. 6.3; Conservative 0; Mismatches
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CGTTAATTCGCGTTCCTC 18

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Matches
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Publication No. US20040123343A1
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APPLICANT:
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                                                                       PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
                                                                                                                                             PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                               FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Chery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                                                                                   APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1209 GTTAATTCACGTTCCTC 1193
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Zyskind, Judith
                                                                                                                                                                                                                                                                                                           Forsyth, R.
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Barbazuk, Brad
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o. US20040029129A1
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94.1%;
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Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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118

GTTAATTCGCGTTCC 104

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; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-996
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                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version SEQ ID NO 996
                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Haselbeck,
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Best Local
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NUMBER OF SEC ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 978
LENGTH: 127
TYPE: DNA
ORGANISM: Enterococcus faecalis
                                                      Query Match
Best Local Similarity
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Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
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                                                                                                                                                                        LENGTH: 128
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                                      15;
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GTTAATTCGCGTTCC 16
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Yamamoto, Robert T
Xu, H. Howard
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Zyskind, Judith W.
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                                  83.3%; Score 15; ilarity 100.0%; Pred. No. Conservative 0; Mismatci
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                                                                        DB 9;
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US-09-815-242-555/c

Sequence

555, Application US/09815242
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LENGTH: 250
TYPE: DNA
ORGANISM: Enterococcus faecalis
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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PRIOR TILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang,
APPLICANT: Zamu
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APPLICATION NUMBER: 60/1.
FILING DATE: 2000-03-07
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Similarity 100.0%; Pred. No. 3.5e+02;
15; Conservative 0; Mismatches 0;
                                                                                                                                         Yamamoto, Robert Forsyth, R.
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Zyskind, Judith
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Malone, Cheryl
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Zyskind, Judith W.
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Trawick, John
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lio, Carlos
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                               60/191,078
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US-10-282-122A-6332
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                                     PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
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SEQ ID NO 531
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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APPLICANT: Zamudio, Carl
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PRIOR FILING DATE: 2000-09-06
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TYPE: DNA
ORGANISM: Enterococcus faecalis
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FILING DATE: 2000-05-23
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
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Malone, Cheryl
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; SEQUENCE DESCRIPTION: SEQ ID NO: 334: US-09-070-927A-334
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US-09-070-927A-334
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; ORGANISM: Enterococcus faecalis
US-10-282-122A-6332
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Best Local Similarity 100.
15; Conservative
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                      Query Match
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 334: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                              STRANDEDNESS: double
                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                        LENGTH: 9212 base pairs
                                                                                                                                                                                                               TELEFAX: (301)
                                                                                                                                                                                                                                     TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steven Barash
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.3%; Score 15;
100.0%; Pred. No.
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                                                                                                                                                                                                                 309-8512
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Score 15;
Pred. No.
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DB 9; Lo
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                  Length 9212;
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Best Local Similarity

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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01153717
US-09-535-459-1371
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US-09-535-459-1371/c
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                                                              Matches
                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 43896
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43896, Application US/10424599
Publication No. US20040031072A1
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SEQ ID NO 1371
LENGTH: 262
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                                                                             Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/535,459
CURRENT FILING DATE: 2000-03-24
Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 2170
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa Thomas J APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLECTIDES ENCODING OR
FILE REFERENCE: PD-1014 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Seilhamer, Jeffrey J. APPLICANT: Delegeane, Angelo M.
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                                                                                                                                        FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_139637C.1
                                                                                                                                                                                              LENGTH: 438
TYPE: DNA
                                                                                                                                                                        ORGANISM: Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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297 CGTAAATTCGCGTTCATC 314
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Stuve, Laura L.
Mullahy, Sara J.
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                                                              Conservative
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                                                                             82.2%;
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                            18
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                                                            Score 14.8; D
Pred. No. 4.8e
0; Mismatches
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Pred. No. 4
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                                                                            4.8e+02
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                                                                                              BB
                                                                                            13;
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                                                                Indels
                                                                                           Length
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                                                                                              438;
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                                                              Gaps
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RESULT 13
US-10-282-122A-20853/c
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; ORGANISM: Drosophila
US-10-255-536-103
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US-10-255-536-103
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                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103
LENGTH: 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 103, Application US/1025536
Publication No. US20030087807A1
GENERAL INFORMATION:
APPLICANT: Greenspan, Ralph J.
TITLE OF INVENTION: Methods for Identifying Compounds for
TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to
TITLE OF INVENTION: Balance and the Perception of Gravity
FILE REFERENCE: P-NI 3864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NO 5E0 ID NOS: 204966 SEQ ID NO 81762
                                                                                                                                                   Matches
                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/255,536
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US/09/669,751
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/168,579
PRIOR FILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: PAT_MRT4530_81256C.1
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                                                                                                                                                                     Local
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                                                                                                                                                                   Similarity
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                                                                                                            CGTTAATTCGCGTTCCTC 18
                                                                         CGTTCATACGCGTTCCTC 86
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Cao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                 Conservative
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                                                                                                                                                               82.2%;
88.9%;
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88.9%;
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                                                                                                                                                Score 14.8; DB 15; Length 650; Pred. No. 5e+02; 0; Mismatches 2; Indels 0
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Pred. No. 5e+02;
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GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Yoskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
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APPLICANT: XU, H:
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/20,078
PRIOR FILLING DATE: 2000-03-21
PRIOR PRILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/257,931
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US-09-815-242-6520/c
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SEQ ID NO 20853
                                                                 APPLICANT:
APPLICANT:
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APPLICANT:
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Publication No. US20040029129A1
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                 APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2001-02-09
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TYPE: DNA
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Local Similarity 88.9%;
es 16; Conservative
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Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr, Grant
Yamamoto, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Forsyth, R.
ION: Prokaryotes ELITRA.011A
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Pred. No. 5.9e+02;
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GENERAL INFORMATION:

APPLICANT: Simpson, Andrew
APPLICANT: Reinach, Fernando
APPLICANT: Setubal, Joao
APPLICANT: Setubal, Joao
APPLICANT: Medianis, Joao
APPLICANT: Mruda, Paulo
FILLE OF INVENTION ISOLATED Genome of Xylella Fastidiosa and Uses Thereof
FILLE REFERENCE: FARESP 202 US (10213376)
CURRENT APPLICATION NUMBER: US/10/297,465A
CURRENT FILLING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: PCT/IB01/01618
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: PCT/IB01/01618
PRIOR FILING DATE: 2001-06-17
PRIOR APPLICATION SIGNION 12
PRIOR FILING DATE: 2001-06-17
PRIOR APPLICATION SIGNION 201-06-17
PRIOR APPLICATION NUMBER: MO/209,906
PRIOR FILING DATE: 2001-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/243,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-12-22
PRIOR PRIOR DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOPTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 6520
LENGTH: 3138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA; ORGANISM: Enterococcus faecalis; FEATURE: ; NAME/KEY: CDS; LOCATION: (1)...(3138)
US-09-815-242-6520
Search completed: October Job time: 83.304 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-10-297-465A-1
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; SEO ID NO 1
; LENGTH: 2731748
; TYPE; DNA
; ORGANISM: Xylella fastidiosa
US-10-297-465A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10297465A Publication No. US20040142413A1
                                                                                                                                                                                                                         Query Match
Best Local S
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                                                                                                  2184289 CGGTATTTCGCGTTCCTC 2184306
                                                                                                                                                                                             y Match 82.2%; Score 14.8; DB 17; Local Similarity 88.9%; Pred. No. 8.6e+02; hes 16; Conservative 0; Mismatches 2;
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Local Similarity 88.9%;
nes 16; Conservative
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                            2004, 08:53:55
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Minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
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                                                                                                                                                                                                                                                                                                                                   Post-processing:
                                                                                                                                                                                                                                                                                                                                                      DB seq length: 0
DB seq length: 2000000000
  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                       27513289 seqs, 14931090276 residues
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18
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Maximum Match 100%
Listing first 45 summaries
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gb est2: *
gb htc: *
gb est3: *
gb est4: *
gb est5: *
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em_gss_pro:*
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gb_gss1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4	c u	c 2	c 1	Result
15.4	15.4	15.4	16.4	Score
85.6	85.6	85.6	91.1	Query Match
402	277	262	667	Query Match Length DB
29	28	28	13	8
CG858920	BH452985	AZ359925	BQ483402	sult Query No. Score Match Length DB ID
CG858920 ZMMBBc026	BH452985 BOHGA60TF	AZ359925 1M0103BO2	BQ483402 WHE3508 B	Description

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12	14	9	12	12	28	14			14		28	10					14	28	28	12	14	29	14	12	10	14	14	12	10	12	12	14	14	13	14	29	29	28	28	28
3061	CA408218	AA941852	S	ω	AQ945783	CB339034	AI946050	AI212546	CB767429	AI869164	0145	E99515	BF490378	AL714174	AJ502973	AA785231	CB066239	AZ991080	AZ991070	BM616169	CB066245	AG081712	0081	2326	5713	0615	B40613	8194	3331	M54381	1228	867	8891	3486	N	1064	AG042918	0855	4478	AZ498171
M130610 pj07a1	CA408218 pk26g02.x	941852 LD27162	вм130858 рј10е01.у	вм130898 рј10h10.у	AQ945783 Sheared D	CB339034 pl37h09.y	AI946050 bs20b03.y	AI212546 x8b12a1.f	CB767429 AMGNNUC:N	AI869164 wl50b04.x		BE995152 UI-M-CGOp	BF490378 AT26843.5	AL714174 AL714174	AJ502973 AJ502973	AA785231 g5h08a1.f			275N0	BM616169 170006871	CB066245 PVBE11E11	AG081712 Pan trogl	CK200815 FGAS00933	BG723264 602690884	BE557132 fk94g09.y	06152	B406133	81942	33312	43811	12280	86745 EST74946	88913 EST7516	34865 BX4	78228 S	ч	8	8556 BONSH38T	H144783 TDGE091T	AZ498171 1M0335P13

ALIGNMENTS

RESULT 1 BQ483402/c LOCUS SOURCE ORGANISM ACCESSION VERSION DEFINITION Triticum aestivum (bread wheat)
Triticum aestivum
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.

1 (bases 1 to 667)
Anderson,O.D. Chao,S., Close,T.J., Crossman,C., Fenton,R.D.,
Lazo,G.R., Nguyen,H.T., Rausch,C.J., Wilson,C., Woo,J. and Zhang,D.
The structure and function of the expressed portion of the wheat
The structure and function of the compassed portion of the wheat
The structure and function of the compassed portion of the wheat в0483402 667 bp mRNA linear EST 03-JJD WHE3508_B09_D18ZS Wheat unstressed root cDNA library Triticum estivum cDNA clone WHE3508_B09_D18, mRNA sequence. BQ483402 BQ483402.1 GI:21319338 EST EST 03-JUN-2002

KEYWORDS

REFERENCE AUTHORS

TITLE

JOURNAL COMMENT Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773 Fax: 5105595818 Service, Pacific

Email: oandersn@pw.usda.gov Sequences have been trimmed

to remove vector sequence and low

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JOURNAL COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
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AZ359925/c
                                                   FEATURES
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243
                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error:
Plate: 0103 row: B column: 02
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss University of Utah Genome University of Utah
                                                                                                                                                                                                                                                                                                                                                                                           plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 bp DNA linear GSS 02-OCT-20
1M0103B02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0103B02 F, genomic survey sequence.
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                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                    308,
                                              quality sequence stop: 262.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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/lab_host="E. coli SOLR"
/clone_lib="Wheat unstressed root cDNA library"
/clone_lib="Wheat unstressed root cDNA library"
/clone_lib="Wheat unstressed root cDNA library"
/note="Tweetor: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(-); Site_l: EcoRI; Site_l: XhoI; Plants
were grown until full tillering stage and root tissue was
collected at Texas Tech Univeristy (Zhang, HT Nguyen
Lab). Total RNA and poly(A) RNA were prepared, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript SK(-) phagemids in the TJ
Close_lab (Close, Fenton) at the University of
California, Riverside. Colony plating, plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg., 20 S. 2030 E., SI.C.
                            1. .262
organism="Mus musculus"
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/tissue_type="Roots"
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94.4%;
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Pred. No. 3.4e+02;
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AUTHORS
TITLE
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BH452985/c
LOCUS
ORIGIN
                                                                                                                                                                                                                                                         FEATURES
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ORGANISM
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Best Local Similarity
                                                                                                                                                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica oleracea
Brassica oleracea
Brassica oleracea
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole genome shotgun sequencing of Unpublished (2001)
Other_GSSs: BOHGA60TR
                                                                                                                                                                                                                                                                           Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, Tel: 301-838-3523 Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH452985.1 GI:17638696 GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH452985 277 bp DNA linear GSS 12-DEC-2001
BOHGA60TF BOHG Brassica oleracea genomic clone BOHGA60, genomic
                                                                                                                                                                                                                                                                                                                              Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BH452985
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwn42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
          /clone_lib="BOHG"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers
                                                                                                                                               /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                            /db_xref="taxon:3712"
/clone="BOHGA60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC1M0103B02"
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94.1%;
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Pred. No. 9.9e+02;
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                     BstXI linkers"
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RESULT 5
AZ498171/c
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SOURCE
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VERSION
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AUTHORS
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CG858920
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Best Local Similarity
Matches 16; Conser
                                                         ORGANISM
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Best Local (
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                                                                                                                                                                  M493 bp DNA linear 1000 plasmid UUGC1M library Mus clone UUGC1M0335P13 F, genomic survey sequence.
     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronz Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J. Sequencing of the maize genome at PGIR (2003c) Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 bp DNA linear GSS 19-NOV-20 DMBBc0267L01f ZMMBBc (EcoRI) Zea mays subsp. mays genomic clone ZMMBBc0267L01 5', genomic survey sequence.
                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG858920.1 GI:38431633
GSS.
                                                                            Mus musculus (house mouse)
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Bharti, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 Frelinghuysen Road, Piscataway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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732 445 5735
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="ZMMBBc0267L01"
/lab_host="E. coli DH10B"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBc (EcoRI)"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="mays"
/db_xref="taxon:4578"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cultivar="B73"
                                                                                                                                GI:10675786
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94.1%;
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Pred. No. 1.1e+03;
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                  musculus genomic
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BH144783
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                                                                                                   VERSION
KEYWORDS
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AUTHORS
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                                                                                                                                                                                                     DEFINITION
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Best Local S
Matches 16
                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0335 row: P column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. We
University of Utah Ge
University of Utah
Rm. 308, Biomedical F
Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                              TDGEO91TH cTOG Lycopersicon esculentum genomic genomic survey sequence.
BH144783
BH144783.1 GI:15200046
GSS.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                               BH144783
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                                                                                                                                                                                                                                                                                                                                                          GTTAATTCGCCTTCCTC 367
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pushed (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complements, to the insert edge to the contract of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/lab_host="E. Coli strain XL10-Gold, T1-resistant,
/lab_host="E. Coli strain XL10-Gold, T1-resistant,
/clone_lb="Mouse 10kb plasmid UUGCIM library"
/clone_"Vector: PWD42nv; Purified genomic DNA from the Jac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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BZ508556.1 GI:27031477
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Class: shotgun.
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tomato demethylated genomic DNA
Insert Length: 1270 Std Error: 0.00
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Contact: CUGI
                         DNA is from a doubled haploid provided by Tom Osborn Seq primer: TF
                                                                                                                                                                                                                                                                                 Contact: Chris Town
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                                                                                                    Email: cdtown@tigr.org
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                                                                                                                                     301-838-3523
                                                                                                                                                                                                      Medical Center Drive,
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/dev gtage="12-14 weeks post harvest"
/lab_host="B.coli JM109"
/clone lib="cTOG"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; This library was made from short EcoRI digested
fragments of the genome of Lycopersicon esculentum ligated
into pBS (SK.). The fragments were cloned into the
methylation restrictive E.coli strain JM109 with the
methylation restrictive E.coli strain JM109 with the
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|mol_type="genomic DNA"
|cultivar="E6203"
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614 GTTAATACGCGTTCCTC
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                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170 Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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AG042918
AG042918.1 GI:16571643
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Totoki,Y., Watanabe,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujiyama,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes (chimpanzee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                            Similarity
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                            GTTAATTCGCGTTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 740)
                                                                                                                                                                                                                                                                                       Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
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                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                     Sequencing: M13Rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Brassica oleracea"
/mol type="genomic DNA"
/strain="TO1000DH3"
/db xref="taxon:3712"
/clone="BONSH38"
                                                                                                                                          /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                        /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone lib="BO_1.6_2_KB tot"
/note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb shea
total DNA inserted into pHOS1 using BstXI linkers"
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                                                                                                                                                                          /sex="male"
                                                                                                                                                                                         clone="PTB-021B05.R"
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                                                                                                                                                                                                                                                            . 740
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                                                             Score 15.4; DB 29
Pred. No. 1.2e+03;
0; Mismatches 1
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Pred. No. 1.1e+03;
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                                                                                               29;
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ORGANISM
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                   322 CGTTCATTCGCGTTCCT 338
Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
                                                                                                                                                                                        SCBFSD2037A01.g SD2 Saccharum 5', mRNA sequence. CA278228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_GSSs: FSAAOB2TR
Contact: Chris Town and K. Meksem
Contact: Chris Town and K. Meksem
The Center of Excellence in Soybean Research, Teaching and
Outreach, Southern Illinois University at Carbondale and Plant
Genomics, The Institute for Genomic Research
Room 176, Ag. Building, Mail Code 4415, Carbondale, IL 62901-4415,
Room 17912 Medical Center Drive, Rockville, MD 20850, USA
Tel: 618 453 3103 and 301-838-353
Fax: 618 453 7457 and 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CG810640 819 bp DNA linear GSS 13-NOV-200
FSAAO82TF LargeInsertGenomicLibrary Fusarium virguliforme genomic
clone KMFV4N19, genomic survey sequence.
CG810640 GI:38264114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

(bases 1 to 819)

Meksem,K., Ishihara,H., Koo,H., Shultz,J., Ali,S., Iqbal,J.,
Lightfoot,D.A. and Town,C.D.

End sequencing of BACs from a fingerprint physical map of the
causative agent of soybean sudden death syndrome, Fusarium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: meksemk@siu.edu; cdtown@tigr.org (URL:
http://Fusariumvirguliform.siu.edu)
Seq primer: TGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             verguliforme
Unpublished (2003)
                                                                                                                                                                    CA278228.1 GI:36001615
                                                                                                                                                                                                                                                               CA278228
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="LargeInsertGenomicLibrary"
/clone lib="LargeInsertGenomicLibrary"
/note="Organ: Hyphae; Vector: pINDIGOBAC5; A single spore
derived culture was used. Hyphae were grown in an
incubator for four days. Nulphae were isolated and embedded
in agarose, restriction digested with Hind III. Large size
DNA fragments were ligated in vector pINDIGOBAC5 and
electro-transformed into DH10B cells."
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| mol_type="genomic DNA"
| fullivar="Monticello"
| db_xref="taxon:232082"
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94.1%;
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Pred. No. 1.2e+03;
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narum officinarum cDNA clone
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a SCBFSD2037A01
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BX434865
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 GTTAATTCGAGTTCCTC 526
                   Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7207.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAK033AB03NM1&cluster=7207.r. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BX434865 Homo sapiens FETAL BRAIN Homo CSODFO12YH19 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
                                                                                                                                                                                                               Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
1 (bases 1 to 908)
1 (M.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: clone distribution through the Brazilian Clone Collection http://www.bcccenter.fcav.unesp.br
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vettore, A.L., da Silva, F.R., K
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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//clone_lib="SD2"
//note="Organ: Developing seeds (small insert library);
//note="Organ: Developing seeds (small insert library);
Vector: pSportl; Site 1: Sall; Site 2: Notl; An
unidirectional cDNA library generated from [Developing
seeds (small insert library)]. cDNA was prepared from
polyA+ mRNA using SuperScript plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
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/db_xref="taxon:4547"
/clone="SCBFSD2037A01"
/lab_host="DH10B"
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94.1%;
gth.invitrogen.com/ InVitroGen Corporation 1600 Genoscope sequence ID : CSOBAKO33AB03NM1.
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Pred. No. 1.2e+03;
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Center (BCCC)
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RESULT 12
CK288913
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG AGA CTA TAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CK288913 921 bp mRNA linear EST 15-DEC-2003
EST751635 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMBK06 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2003)
Other_ESTs: EST751636
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Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
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tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (9seudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-cligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
                                                                                                                                                                                                               /clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSport6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from NIcotiana benthamiana
                                                                                                                                                                                                                                                                                                                       /tissue_type="abiotic and biot:
callus tissue and root tissue"
/lab_host="DH10B-TonA"
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/clone="CS0DF012YH19"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
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/mol_type="mRNA"
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'clone="NBMBK06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Nicotiana benthamiana"
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94.1%;
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Pred. No. 1.2e+03;
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REFERENCE
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RESULT 14
BP512280/c
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Best Local :
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                                                                                                               2 GTTAATTCGCGTTCCTC 18
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1 (bases 1 to 968)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana
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EST749467 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBMB430 5'
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Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                    tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length" /note="Vector: pCWVSport6:1; Site_1: EcoRI; Site_2: NotI; supplier: RNA was isolated from Nicotiana benthamiana
                                                                                                                                                                                                                                                                                 these tissues and pooled in approximately equal molar amounts."
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/lab_host="DH10B-TonA"
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/db_xref="taxon:4100"
/clone="NBMB430"
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Pred. No. 1.3e+03;
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DEFINITION

BP512280 Hydra magnipapillata cDNA library Hydra magnipapillata

EST 16-SEP-2003

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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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VERSION
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Best Local Similarity
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                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1278)

18 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

10 Unpublished (1999)

11 Contact: Robert Strausberg, Ph.D.

12 Email: cgapbs-r@mail.nih.gov

13 Tissue Procurement: Invitrogen

14 CDNA Library Preparation: Life Technologies, Inc.

15 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

16 DNA Sequencing by: Agencourt Bioscience Corporation

17 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

18 http://image.llnl.gov

19 Plate: LLAM12361 row: g column: 03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Jung Shan Hwang
Center for Information Biology and DNA Data Bank of Japan
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-55-981-6847(ex.6898)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP512280 T GI:34778413 EST.
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Hydra EST project
Unpublished (2003)
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Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM543811.1 GI:18774526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTTAATTCGCGTCCCT 403
                                                              quality sequence start: 8 quality sequence stop: 548.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jhwang@lab.nig.ac.jp, URL:http://www.cib.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Hydra magnipapillata"
/mol_type="mRNA"
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/dev_stage="adult budding stage"
/clone_lib="Hydra magnipapillata cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _xref="taxon:6085"
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Pred. No. 1.3e+03;
0; Mismatches 1;
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Query Match
                                                                                                                          /lab_host="DH10B"
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/clone lib="NIH MGC 125"
/clone lib="NIH MGC 125"
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/note="Corpan: ovaries, from females ranging in age from 38 to
f three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
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   85.6%;
94.1%;
Score 15.4; DB 12
Pred. No. 1.3e+03;
                                 DB 12;
                              Length 1278;
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밁 Ś 794 CGTTACTTCGCGTTCCT 810 CGTTAATTCGCGTTCCT 17

ORIGIN

Matches

16;

Conservative

<u>,</u>

Mismatches

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Best Local Similarity

Search completed: October Job time: 260.333 secs ۳, 2004, 08:01:51 This Page Blank (Uspto)

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Maximum Match 1004
Listing first 5000 summaries
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1: gb_ba:*
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18
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AF38703
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RESULT 1
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Sequence 50 AR206444 AR206444.1

GI:21505047

AR206444

18 bp 50 from patent US 6372430.

DNA

linear

PAT 20-JUN-2002

ALIGNMENTS

Unknown. Unclassified. Unknown a

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RESULT 3
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Patent: JP 2001525665-A 50 11-DEC-2001;
Patent: JP 2001525665-A 50 11-DEC-2001;
Patent: JP 2001525665-A 50 11-DEC-2001;
PATENT OF THE UNITED STATES OF AMERICA AS REPRESENTED THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE
                                                                                                                                                                                                                                                                                 Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

1 (bases 1 to 18)

Morrison, C.J., Reiss, E., Aidorevich, L. and Choi, J.S.

Mucleic acids for detecting Aspergillus species and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 18)
Morrison, C.J., Reiss, E., Aidorevich, L. a
Nucleic acids for detecting Aspergillus
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Nucleic acids
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Patent: US 6372430-A 50 16-APR-2002;
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02-MAY-1997 US 60/045400
CHRISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG
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                                                                                                                                                                                                                                                             Location/Qualifiers.
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Fusarium oxysporum f. sp. fragariae
Fusarium oxysporum f. sp. fragariae
Eukaryota, Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           API62899 335 bp DNA linear PLN 04-AUG-1999 Fusarium oxysporum f. sp. fragariae 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-JUN-1999) Biology, SangMyung University, Dong, Chong Ro-Gu, Seoul 110-743, Korea Location/Qualifiers
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and 28S ribosomal RNA gene, partial sequence.
AF162898
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                                                                                                                                                                                                                             Chong Ro-Gu, Seoul 110-
Location/Qualifiers
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                                                                                           forma_
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 /product="internal transcribed spacer
278. .>335
                                     /product="5.8S ribosomal RNA" 129. .277
                                                                                                                                                    /organism="Fusarium oxysporum
/mol_type="genomic DNA"
/strain="MAFF 744009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Fusarium oxysporum
/mol_type="genomic DNA"
/strain="MAFF 744001"
                                                                                               /note="forma specialis: fragariae
forma_specialis: fragariae"
                                                                                                                                 db_xref="taxon:100903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="28S ribosomal RNA"
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Fusarium
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Pusarium oxysporum f. sp. raphani
Eusaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (28-JUN-1999) Biology,
Dong, Chong Ro-Gu, Seoul 110-743,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusarium oxysporum f. sp. raphani 5.8S ri
sequence; internal transcribed spacer 2,
ribosomal RNA gene, partial sequence.
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                                    Eusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

1 (bases 1 to 338)
                                                                                                                                                      Fusarium oxysporum strain FS-1 5.8S ribosequence; internal transcribed spacer 2, ribosequal RNA gene, partial sequence.
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 Use of lig
            Tooley, P.W., Hatziloukas, E., Use of ligase chain reaction
                                                                                                      Fusarium oxysporum
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                                                                                                                                                                                                                                                                                                                                                                                                                                     product="5.8S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mol_type="genomic DNA"
db_xref="taxon:96318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Fusarium oxysporum f.
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in potatoes
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2, complete sequence;
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               . and Carras, M.M of Phytophthora
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                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                     gene, partial sequence; and
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A gene, partial
                                                                                                                                                                                                PLN 25-OCT-2002
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TITLE
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Best Local S
Matches 18
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Tooley,P.W., Hatziloukas,E., Scott,D.L. Jr. and Carras,M.M. Direct Submission
Submitted (22-JAN-2001) Agricultural Research Service, U.S. Department of Agriculture, 1301 Ditto Ave., Ft. Detrick, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
AY383320
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Pusarium oxysporum f. sp. vanillae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
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                                                                                                                                                                                                                                                                                       Submitted (08-SEP-2003) Dept.
University, Long Tou Street, I
Location/Qualifiers
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Wang, Y.Y., Whitehead, M.,
Direct Submission
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Wang,Y.Y., Whitehead,M.,
Fusarium oxysporum f. sp
ITS 2 sequence
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larity 100.0%;
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spacer 2, and 28S ribosomal RNA"
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/mol_type="genomic [
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                                                                                                                                 /product="5.88 ribosomal RNA"
275. .>426
                                                                                                                  /product="internal transcribed
                                                                                                                                                                                                                                                               organism="Fusarium oxysporum"
                                                                                                                                                                                                     note="forma_specialis: vanillae"
                                                                                                                                                                           product="internal transcribed
                                                                                                                                                                                                                     db_xref="taxon:247126"
                                                                                                                                                                                                                                   mol_type="genomic DNA" isolate="DL-1-1"
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Pred. No.
                                                            Score 18; DB
Pred. No. 26;
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Kunming, Yunnan 650201, E
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RESULT 9
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ORGANISM
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VERSION
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AF502842/c
                                 REFERENCE
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Best Local S
Matches 18
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                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                    82
2 (bases 1 to 441) Wang, Y.Y., Whitehea and Li, X.
                                                                                                                                                                Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Fungi; Ascomycota; mitosporic Hypocreales; Fusari
                                                                                                                                                                                                                                                                                         A41 bp DNA linear PLN 07-OCT FUSARIUM OXYSBOTUM isolate DL-2-7 internal transcribed spacer partial sequence; 5.88 ribosomal RNA gene, complete sequence; internal transcribed spacer 2, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 430)
Gilbert,G.S., Garbelotto,M., Chapela,I.,
Dreyfuss,M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF502842 430 bp DNA linear PLN 13-MAY-2002 Leaf litter ascomycete strain its331 isolate 1000502849 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial
                                                Unpublished
                                                                 Fusarium oxysporum isolate DL-2-7
5.8S ribosomal RNA gene and intern
                                                                                                                     Wang, Y.Y., Whitehead, M., Zhu, Y.Y.,
                                                                                                                                     Fusarium oxysporum complex.

1 (bases 1 to 441)
                                                                                                                                                                                                                       Fusarium oxysporum
                                                                                                                                                                                                                                                              AY387703.1
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California, Santa Cruz, 1156 High St., Santa Cruz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 430)
Gilbert, G.S., Garbelotto, M., Chapela, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biogeography of leaf litter
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AF502842
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leaf litter_ascomycete strain its331
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTTAATTCGCGTTCCTC 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribosomal RNA and internal transcribed spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="leaf litter ascomycete
/mol_type="genomic DNA"
/strain="its331"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains internal transcribed spacer 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /specific_host="Miconia te"
/db_xref="taxon:194114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            country="Puerto Rico"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /isolate="1000502849"
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                 Whitehead, M.,
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Pred. No.
                 Zhu,Y.Y.,
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                                                                     internal
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                                                                   internal transcribed spacer 1, nal transcribed spacer 2 sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8;
                                                                                                                     Burns, A.,
                 Burns, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain its331"
                                                                                                                     Hocking, T.,
                 Hocking, T.,
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2"
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                                                                                                                     Ruan, X.Y.
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RESULT 10
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Best Local Similarity
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   l Similarity
18; Conserv
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A45 bp DNA linear PLN 04-OCT-200 Fusarium oxysporum f. sp. vanillae internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

AY380575
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                                                                                                                                                                                                                                                                                               Submitted (03-SEP-2003) Plant Pathology, Yunnan Agricultural University, Longtou Street, Kunming, Yunnan 650201, Peoples
                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 445)
Wang, Y.Y., Whitehead, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusarium oxysporum f. sp. vanillae Fusarium oxysporum f. sp. vanillae
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                                                                                                                                                                                                                                                                                Republic
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                                                                                                                                                                                                                                                                                                                                                                                                           vanillae
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang, Y.Y., Whitehead, M., Burns, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY380575.1 GI:37039595
                                                                                                                                                                                                                                                                                University, Longtou Street, Kunming, Republic of China
                                                                                                                                                                                                                                                                                                                                               Ruan, X.Y
                                                                                                                                                                                                                                                                                                                                                                                                                           ITS1,
                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 usarium oxysporum complex.
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                                                                                           /product="5.8S ribosomal RNA"
294. .>445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="5.8S ribosomal RNA" 294. .>441
                                                                                                                                                                                                     /organism="Fusarium
/mol_type="genomic I
/isolate="HK-5a-4"
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="DL-2-7"
                                                                             product="internal transcribed"
                                                                                                                           product="internal transcribed spacer
                                                                                                                                                                     note="forma_specialis:
                                                                                                                                                                                     db_xref="taxon:247126"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="internal transcribed
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100.0%; Score 18; DB
100.0%; Pred. No. 26;
tive 0; Mismatches
                                                                                                                                                           . 135
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Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                            Burns, A.,
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DNA"
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                                 DB 8;
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                                Length 445;
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Matches

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AY387698
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AUTHORS
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AY387699
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VERSION
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Best Local
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                                                                                                                                                                                                                                                                                               327
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Fusarium oxysporum f. sp. vanillae
Fusarium oxysporum f. sp. vanillae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusariu
Fusarium oxysporum complex.
1 (bases 1 to 445)
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Molecular investigation of isolates of Fusarium oxysporum in
relation to the control of root rot disease in vanilla plani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-SEP-2003) Department of Plant Pathology, Plant Protection, Yunnan Agricultural University, Long Kunming, Yunnan 650201, P. R. China Location/Qualifiers
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Wang, Y.Y., Whitehead, M., Zhu, Y.Y.,
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Wang, Y.Y., Whitehead, M.,
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Fusarium oxysporum f. sp. vanillae
Fusarium oxysporum f. sp. vanillae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari
Fusarium oxysporum complex.
                                                                                                                                                    AY387699 445 bp DNA linear PLN 07-OCT-2 Pusarium oxysporum f. sp. vanillae isolate DL-4b internal transcribed spacer 1, partial sequence; 5.85 ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="5.8S ribosomal RNA" 294. .>445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="internal transcribed
136. .293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Fusarium oxysporum
/mol type="genomic DNA"
/isoTate="ML-8-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="forma_specialis: vanillae"
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            misc_RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-SEP-2003) Department of Plant Pathology, Plant Protection, Yunnan Agricultural University, Long Kunming, Yunnan 650201, P. R. China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
2 (bases 1 to 445)
Wang, Y.Y., Whitehead, M., Zhu, Y.Y.,
                                                                                                                                                                                                                                                                                                                       Eusarium oxysporum
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

1 (bases 1 to 445)
1 "" """" """ """ " Y Y Burns.A., Hocking,T., Ruan,X.Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcribed spacer 1, 5.8S ril
transcribed spacer 2 sequence
                                                                                                            Submitted (10-SEP-2003) Department of Plant Pathology, Plant Protection, Yunnan Agricultural University, Long Kunming, Yunnan 650201, P. R. China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AY387702 445 bp DNA linear PLN 07-OCT
Fusarium oxysporum isolate ML-7-1 internal transcribed spacer
partial sequence; 5.8S ribosomal RNA gene, complete sequence;
internal transcribed spacer 2, partial sequence.
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Wang,Y.Y., Whitehead,M., Zhu,Y.Y.,
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/product="internal transcribed spacer 1"
                           /db_xref="taxon:5507"
                                               mol type="genomic DNA"
isolate="ML-7-1"
                                                                              organism="Fusarium
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RESULT 15
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AY387705

AY387705

AY387705

Pusarium oxysporum isolate ML-5-2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

AY387705

AY387705.1 GI:37362910
                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-SEP-2003) Department of Plant Pathology, Plant Protection, Yunnan Agricultural University, Long Kunming, Yunnan 650201, P. R. China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusarium oxysporum isolate ML-8-4 internal transcribed spacer partial sequence; 5.8S ribosomal RNA gene, complete sequence; internal transcribed spacer 2, partial sequence.
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1 (bases 1 to 445)
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19,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T.,
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294. .>445
                                                                                                                                                                                                                                                                                                 product="internal transcribed"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                            Fusarium oxysporum isolate 12-117 internal transcribed spacer partial sequence; 5.8S ribosomal RNA gene, complete sequence; internal transcribed spacer 2, partial sequence.
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                                                                                                                                                                                               Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian 350003,
                                                                                                                                                                                                                              Liu, B., Zhu, Y.J.,
Direct Submission
                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium, oxysporum complex.
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                                                                                                                                                                                                                                                                                                                                                Fusarium oxysporum
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and Chen,J.B.
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5.8S ribosomal RNA gene and internal transcribed spacer
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1 (bases 1 to 445)
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                                                          /specific_host="pease plant"
/db_xref="taxon:5507"
                 /product="internal transcribed
139. .296
                                                                                                 /mol_type="genomic DNA'
/isolate="12~117"
                                                                                                                                                                Location/Qualifiers
/product="5.
                                                                                                                              organism="Fusarium oxysporum"
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/isolate="ML-5-2"
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447 bp DNA linear PLN 20-JUL-200 Fusarium oxysporum isolate 12-132 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu, B., Zhu, Y.J., Ling, Y.Z. and Cao, Y. Direct Submission Submitted (28-UUR-2004) Biotechnology Center, Fuj. Agricultural Sciences, No. 247 Wusi Road, Fuzhou, P.R. China
                                                                                                                                                 AY667490 447 bp DNA linear PIN 20-UUL-200 Fusarium oxysporum isolate 12-136 internal transcribed spacer 1, partial sequence; 5.85 ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium oxysporum complex.

1. (bases 1 to 447)
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llarity 100.0%;
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Zhu, Y.J., Ling, Y.Z. and Cao, Y
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isolate="12-132"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Fusarium
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                                               Hypocreales; Fusarium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 bp DNA linear PLN 07-OCT-2003 Fusarium oxysporum isolate MJD-2-2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence. AX387701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-JUN-2004) Biotechnology Center, Fujian Acac
Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
18; Conserv
                                                                                                                                                                                                                                             Submitted (10-SEP-2003) Department of Plant Pathology, Plant Protection, Yunnan Agricultural University, Long Kunming, Yunnan 650201, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                          Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., and Kong,Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusarium oxysporum

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari
                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 447)
Wang, Y.Y., Whitehead, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY387701.1 GI:37362906
                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                              Fusarium oxysporum isolate MJD-2-2
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/db_xref="taxon:5507"
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/isolate="12-136"
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/mol_type="genomic DNA"
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                                                                                    /product="5.8S ribosomal RNA" 278. .>447
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                                                                                                                                                                      /organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="MJD-2-2"
                                                                                                                                                                                                                            Location/Qualifiers
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                                                                      /product="internal transcribed
                                                                                                                                                      db_xref="taxon:5507"
                                                                                                                              product="internal transcribed
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             100.0%;
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                                                                                                                                                                                                                                                                              455 bp DNA linear PLN 08-JUN-1 Fusarium oxysporum strain CBS 171.31 internal transcribed spacer region ITS1, 5.8S ribosomal RNA gene, and internal transcribed spacer region ITS2. includes the 5.8S gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (31-MAY-1995) Artie Duggal, Forestry,
Toronto, 33 Willcocks St., Toronto, Ontario M5S
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

1 (bases 1 to 455)
                                                                                                                                                                       Fusarium oxysporum

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Eukaryota; Fungi; Hypocreales; mitosporic Hypocreales; Fusarium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                 Toronto,
                                                                                                 Submitted
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                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="5.8S ribosomal RNA"
305. .455
/note="internal transcribed spacer region; ITS2"
                                                                                 1 (31-MAY-1995) Artie Duggal,
33 Willcocks St., Toronto, O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L. .455
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/strain="CBS 171.31"
                                                           33 Willcocks St., To
Location/Qualifiers
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strain="DAOM 213391"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="internal transcribed spacer region; ITS1"
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Ontario M5S
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transcribed spacer
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3B3, Canada
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AF440529 LOCUS

DEFINITION

AF440529 Fusarium oxysporum 5.8S ribosomal RNA

456 bp DNA linear PLN 24-SEP-2003 isolate 35RK-14 internal transcribed spacer 1, gene, and internal transcribed spacer 2,

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SOURCE
ORGANISM
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AF440527
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 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF440527 456 bp DNA linear PLN 24-SEP-2003 Fusarium oxysporum isolate 14RK-11 internal transcribed spacer 1, 5.85 ribosomal RNA gene, and internal transcribed spacer 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGTTAATTCGCGTTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete sequence. AF440527
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

1 (bases 1 to 456)
                                                                                                                                                                                                                                                                                                        Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                                                                                   from tomato plants
Can. J. Bot. 80 (3), 271-279 (2002)
2 (bases 1 to 456)
Bao,J.R., Fravel,D.R. and Lazarovits,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusarium oxysporum Fusarium oxysporum
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                           1 CGTTAATTCGCGTTCCTC 18
                                                          18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                             Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
                                                                      Similarity
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 CGTTAATTCGCGTTCCTC 356
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                                                          Conservative
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/note="The fungus was
Wollenweber H.W. from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="internal transcribed spacer region; ITS1"
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/mol_type="genomic n
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isolate="14RK-11"
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Pred. No.
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Pred. No.
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Mismatches
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                                                             Mismatches
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                                                                             Direct Submission
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS,
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS,
                                                                                                                                         from tomato plants
Can. J. Botc. 80 (3), 271-279 (2002)
2 (Dases 1 to 456)
Bao,J.R., Fravel,D.R. and Lazarovits,G.
                                                                                                                                                                                                                                                                      Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

1 (bases 1 to 456)
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(can. J. Bot. 80 (3), 271-279 (2002)
(bases 1 to 456)
Bao,J.R., Fravel,D.R. and Lazarovits,G.
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1 (bases 1 to 456)
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AF440531
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                                                                     Baltimore Ave, BARC-West, Be.
Location/Qualifiers
                                                                                                                                                                                                                   Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
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                                                                                                                                                                                                                                                     Bao, J.R., Fravel, D.R., O'Neill, N.R., Lazarovits, G.
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Similarity 100.0%;
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/mol_type="genomic DNA"
/isolate="35RK-14"
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="44RK-35"
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Pusarium oxysporum
Eukaryota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

1 (bases 1 to 456)
sequence.
AF440534
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                         AF440534 456 bp DNA linear PLN 24-SEP FUSATIUM oxysporum isolate AL22 internal transcribed spacer 1, ribosomal RNA gene, and internal transcribed spacer 2, complete
                                                                                                                                                                                      18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from tomato plants
can. J. Bot. 80 (3), 271-279 (2002)
2 (bases 1 to 456)
Bao,J.R., Fravel,D.R. and Lazarovits,
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306. .456
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isolate="73RK-1"
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                                                                                                                 Submitted (29-OCT-2001) Vegetable Laboratory, U Baltimore Ave, BARC-West, Beltsville, MD 20705,
                                                                                                                                                                    from tomato plants
Can. J. Bot. 80 (3), 271-279 (2002)
2 (bases 1 to 456)
Bao,J.R., Fravel,D.R. and Lazarovits,G.
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Fusarium oxysporum isolate DEH1 internal transcribed spacer 1, i
ribosomal RNA gene, and internal transcribed spacer 2, complete
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Location/Qualifiers
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                                                                                                  Baltimore Ave, BARC-West, Bel
Location/Qualifiers
                                                                                                                                                                                                                                     Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
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                                                                                                                                                     Direct Submission
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Fusarium oxysporum
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AF440539
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n. J. Bot. 80 (3), 271-279 (2002)
(bases 1 to 456)
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                                 /mol_type="genomic DNA"
/isolate="DEH1"
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   organism="Fusarium oxysporum"
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isolate="AL22"
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Best Local S
Matches 18
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TITLE
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Best Local Similarity
Matches 18; Conserv
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Fusarium
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Fusarium
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Direct Submission
Submitted (29,0CT-2001) Vegetable Laboratory, US
Baltimore Ave, BARC-West, Beltsville, MD 20705,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomy
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Fusarium oxysporum complex.
1 (bases 1 to 456)
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Can. J. Bot. 80 (3), 271-279 (2002)
2 (bases 1 to 456)
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ilarity 100.0%;
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oxysporum isolate DEH2 internal transcribed spacer 2,
1 RNA gene, and internal transcribed spacer 2,
                                              456 bp DNA linear PLN 24-SEP-2003 oxysporum isolate Fo47 internal transcribed spacer 1, 5.8S l RNA gene, and internal transcribed spacer 2, complete
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306. .456
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/isolate="DEH2"
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            GI:18034410
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Pred. No. 26;
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                                                                                                                                Direct Submission
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Raltimore Ave, BARC-West, Beltsville, MD 20705, USA
                                                                                                                                                                                     from tomato plants

Can. J. Botc. 80 (3), 271-279 (2002)

2 (Dases 1 to 456)

Bao,J.R., Fravel,D.R. and Lazarovits,G.
                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

1 (bases 1 to 456)
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Fusarium oxysporum isolate IA7 i
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Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum from tomato plants
Can. J. Bot. 86 (3), 271-279 (2002)
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Bao,J.R., Fravel,D.R. and Lazarovits,G.
                                                                                                                                                                                                                                                      Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ribosomal RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berkum, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van
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Conservative
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/mol_type="genomic DNA"
/product="internal transcribed spacer
148. .305
                                                            /mol_type="genomic
/isolate="IA7"
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                                                                                          organism="Fusarium oxysporum"
                                                                                                                        ocation/Qualifiers
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                                           xref="taxon:5507"
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                                                                            DNA"
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Fusarium oxysporum Fusarium oxysporum
                                                                                 AF440563 456 bp DNA linear PLN 24-SEP Fusarium oxysporum isolate SA70 internal transcribed spacer 1, ribosomal RNA gene, and internal transcribed spacer 2, complet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 456)
Bao,J.R., Fravel,D.R. and Lazarovits,G
Direct Submission
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1 (bases 1 to 456)
Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF440561 456 bp DNA linear PLN 24-8 Fusarium oxysporum isolate PEI1 internal transcribed spacer ribosomal RNA gene, and internal transcribed spacer 2, compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
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                                          AF440563.1
                                                        AF440563
                                                                     sequence.
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Can. J. Bot. 80 (3), 271-279 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Fusarium oxysporum"
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isolate="PEI1"
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Pred. No. 26;
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d spacer 1, 5.8S
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1 spacer 1, 5.8S
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18; Conserv
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(can. J. Bot. 80 (3), 271-279 (2002)

( bases 1 to 456)

Bao, J.R., Fravel, D.R. and Lazarovits, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G.
Berkum,P.
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1 (bases 1 to 456)
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
                                                                                                                                              Direct Submission
Direct Submission
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, Submitted (29-OCT-2001) Vegetable Laboratory, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                     AF440533 457 bp DNA linear PLN 24-SEP-
Fusarium oxysporum isolate ALO1 internal transcribed spacer 1,
ribosomal RNA gene, and internal transcribed spacer 2, complete
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Location/Qualifiers
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                                                                                                                                                                                                from tomato plants
Can. J. Botc. 80 (3), 271-279 (2002)
2 (bases 1 to 457)
Bao, J.R., Fravel, D.R. and Lazarovits, G.
                                                                                                                                                                                                                                                                                             Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G.
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|mol_type="genomic DNA"
  /product="5.8S ribosomal RNA"
307. .457
                                                                                   /organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="AL01"
                                                                 db_xref="taxon:5507"
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                                           product="internal transcribed spacer
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Fusarium oxysporum isolate Litom internal transcribed
5.8S ribosomal RNA gene, and internal transcribed space
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
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Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetės;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
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                                                                                                           Fusarium oxysporum
                                                                                                                                                                                                                AF440560
                                                                                                                                                                                                                                            complete sequence.
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1 (bases 1 to 457)
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/mol_type="genomic DNA"
/isolate="CS-20"
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Pred. No.
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Pred. No.
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Location/Qualifiers
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                                                                                                                                                                                                         Direct Submission
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                              from tomato plants

Can. J. Bot. 80 (3), 271-279 (2002)

Can. Dases 1 to 457)

Bao,J.R., Fravel,D.R. and Lazarovits,G.
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

1 (bases 1 to 457)
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457 bp DNA linear PLN 24-SEP-;
Fusarium oxysporum isolate PEI3 internal transcribed spacer 1, 9
ribosomal RNA gene, and internal transcribed spacer 2, complete
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Can. J. Bot. 80 (3), 271-279 (2002)
2 (bases 1 to 457)
Bao,J.R., Fravel,D.R. and Lazarovits,G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
AF440562
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307. .457
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Pred. No. 26;
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d spacer 1, 5.8S
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Fusarium oxysporum f. sp. vasinfectum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                          l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-MAR-1998) Soil, Plant and Ecological Science Division, Lincoln University, P.O. Box 84, Canterbury, New On Apr 16, 1998 this sequence version replaced gi:3025822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF055220 458 bp DNA linear PLN 29-JUN-2000 Fusarium oxysporum strain FO 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dodd-Wilson,S.L., Crowhurst,R.N., Rodrigo,A.G. and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 458)
Dodd,S.L., Crowhurst,R.N., Rodrigo,A.G., Samuels,G.J., Hill,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari Fusarium oxysporum complex.

1 (bases 1 to 458)
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Fusarium oxysporum
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2 (bases 1 to 458)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Stewart, A.
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                                                                                                                                                             CGTTAATTCGCGTTCCTC 362
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                                                                                                                                                                                                                                                                                                      /product="internal transcribed
/note="ITS-2"
                                                                                                                                                                                                                                                                                                                                                    'product="5.8S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:5507"
/note="pathogen of sq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'mol_type="genomic DNA"
'strain="FO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Fusarium oxysporum"
                                                                                                                                                                                                                                                                                                                                                                                                    product="internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                   product="18S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                   note="ITS-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Direct Submission
Submitted (20-MAR-2003) Molecular Markers Lab., Plant Pathology
Research Institute, 9-Gmaa St., Giza, 002 12619, Egypt
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusarium oxysporum f. sp. vasinfectum
Fusarium oxysporum f. sp. vasinfectum
Eusarium oxysporum f. sp. vasinfectum
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                                                                 Fusarium oxysporum
Fusarium oxysporum
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

1 (bases 1 to 496)
Gure,A., Wahlstrom,K. and Stenlid,J.
Diversity of Fungi Associated with Seeds of Tropical Forest Trees
Podocarpus falcatus and Prunus africana
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AY208788 496 bp DNA linear PLN 30-JUL-: Fusarium oxysporum isolate Po23 internal transcribed spacer 1, i ribosomal RNA gene, and internal transcribed spacer 2, complete
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ITS sequence reg
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3 (bases 1 to 496)
Gure, A. and Stenlid, J.
Direct Submission
Submitted (30-DEC-2003) Forest Mycology & Pathology, Swedish
University of Agricultural Sciences, Ulls vag 26A, Uppsala, Uppland
                                                                                         Direct Submission
Submitted (30-DEC-2002) Forest Mycology & Pathology, Swedisl
University of Agricultural Sciences, Ulls vag 26A, Uppsala,
750 07, Sweden
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Abd-Elsalam, K.A.
                                                                                                                                                                2 (bases 1 to 496)
Gure, A. and Stenlid, J.
                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
AY208788
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121. .240
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_xref="taxon:61374"
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REMARK
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AY243058
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Ascomycete sp. Dune17 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence update by submitter On Dec 30, 2003 this sequence Location/Qualifiers
                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        750 07, Sweden
                                                                                                                                                                                                                                                                                                                                          Submitted (24-FEB-2003) Ecology University of California, Santa
                                                                                                                                                                                                                                                                                                                                                                  Gambetta, G., Gilbert, G.S. and Parker, I.M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota.
1 (bases 1 to 497)
Beckstead, J. and Parker, I.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ascomycete sp. Dune17 ascomycete sp. Dune17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
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 CGTTAATTCGCGTTCCTC
                         CGTTAATTCGCGTTCCTC 18
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                                                  Conservative
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                                                                                                                              /product="5.8S ribosomal RNA" 279. .>497
                                                                                                                                                                                         Bay, California"
/specific_host="Ammophila arenaria"
/db_xref="taxon:227272"
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unsterilized soil collected from Dune Beach, I
                                                                                                                                                                                                                                                            /organism="ascomycete sp. Dune17"
/mol_type="genomic DNA"
/strain="Dune17"
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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isolate="Po23"
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                                                                                                                   /product="internal transcribed
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                                                                 Score 18;
Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                              AY262831 PLN 04-MAY-2003 Push linear PLN 04-MAY-2003 Pushrium oxysporum f. sp. vasinfectum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusarium oxysporum f. sp. vasinfectum
Fusarium oxysporum f. sp. vasinfectum
Fusarium oxysporum f. sp. vasinfectus;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Pusari
                                                                                                                                                                      Pusarium oxysporum f. sp. vasinfectum
Fusarium oxysporum f. sp. vasinfectum
Eusarium oxysporum f. sp. vasinfectum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 501)
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AY247553
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              Direct Submission
Direct Submission
Submitted (27-MAR-2003) Molecular Markers Lab.,
Submitted (27-MAR-2003) Molecular Markers Lab.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-MAR-2003) Biological Perry Road, Exeter, Devon EX4 4QG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection and quantification of Rhizoctonia solani in soil
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1 (bases 1 to 501)
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                                                                           2 (bases 1 to 501)
Abd-Elsalam, K.A.
                                                                                                                                     Molecular diagonastic of Fusarium oxysporium f.sp. vasinfectum
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                                                                                                                 Unpublished
                                                                                                                                                          Abd-Elsalam,K.A.
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complement(<1. .>501)
/note="contains internal transcribed spacer 1,
ribosomal RNA, and internal transcribed spacer
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Fusarium oxysporum f. sp./mol_type="genomic_DNA"
/isolate="BANGD12/B2"
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Location/Qualifiers
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Pred. No.
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AY354386
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Fusarium oxysporum f. sp. radicis-lycopersici
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium oxysporum complex.
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                                                                                                                                                                                                                                                                                                                                                                                Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs Span. J. Agric. Res. 1 (3) (2003) In press

2 (bases 1 to 501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence; and AY354386
                                                                                                                                                                                                                                                                                                                                                                                                                                               Cifuentes, D.
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                                                                                                                                                                                                                                                                                                                                      Direct Submission
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/mol_type="genomic DNA"
/db_xref="taxon:61374"
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                                                                                                                        /product="18S ribosomal RNA"
29. .175
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              /product="28S
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#85. .>501
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176. .333
                                                                                                                                                              /note="forma_specialis: radicis-lycopersici"
                                                                                                                                                                                                 /specific_host="tomato"
/db_xref="taxon:61372"
                                                                                                                                                                                                                               /strain="Forl-12"
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Pusarium oxysporum f. sp. dianthi
Pusarium oxysporum f. sp. dianthi
Eukaryota, Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium
Hypocreomycetidae; Hypocreales; Mitosporic Hypocreales; Hypocreales; Mitosporic Hypocreale
AY354389 501 bp DNA linear Fin 15-5 Fusarium oxysporum f. sp. dianthi 18S ribosomal RNA gene, pa sequence; internal transcribed spacer 1, 5.8S ribosomal RNA and internal transcribed spacer 2, complete sequence; and 28
                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-JUL-2003) Biotechnology, (Murcia) 30150, Spain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetic relationships among seven specialized oxysporum determined by DNA sequencing of the Span. J. Agric. Res. 1 (3) (2003) In press
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485. .>501
/product="28S ribosomal RNA"
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29. .175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /specific_host="carnation"
/db_xref="taxon:42551"
/country="Spain"
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/mol_type="genomic DNA"
/strain="Sur-10"
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Genetic relationships among seven specialized oxysporum determined by DNA sequencing of the Span. J. Agric. Res. 1 (3) (2003) In press 2 (bases 1 to 501)
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Pusarium oxysporum f. sp. dianthi
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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AY354389.1 GI:34559394
Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs Span. J. Agric. Res. 1 (3) (2003) In press 2 (bases 1 to 501)
                                                                                                               Fusarium oxysporum f. sp. melonis
Fusarium oxysporum f. sp. melonis
Fusarium oxysporum f. sp. melonis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

1 (bases 1 to 501)
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                                                                                Cifuentes, D.
                                                                                                   Arroyo-Garcia,R.,
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/note="forma_specialis:
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                                                                                                   Cenis, J.L.,
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                                                                                                     Tello, J., Martinez-Zapater, J.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 501;
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ACCESSION
VERSION
KEYWORDS
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AY354393
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusarium oxysporum f. sp. melonis 185 ribosomal RNA gene, paequence; internal transcribed spacer 1, 5.85 ribosomal RNA and internal transcribed spacer 2, complete sequence; and 28 ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                Genetic relationships among seven specialized oxysporum determined by DNA sequencing of the Span. J. Agric. Res. 1 (3) (2003) In press
                                                                                                                                                                                                                                                                                                                                                  Fusarium oxysporum f. sp. melonis
Fusarium oxysporum f. sp. melonis
Fusarium oxysporum f. sp. melonis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

1 (bases 1 to 501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cifuentes, D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-JUL-2003) Biotechnology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M.
                                                                                                                                                                                   Submitted (29-JUL-2003) Biotechnology, IMIDA,
                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                  Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M.
                                                                                                                                                                                                                                                                                                                      Cifuentes, D.
                                                                                                                                                                                                                                                                                                                                      Arroyo-Garcia, R.,
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                                                                                                                                                                     (Murcia)
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29. .175
/note="forma_specialis: melonis"
<1. .28</pre>
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i85. .>501
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.76. .333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol_type="genomic DNA"
strain="ATCC 28858"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="28S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="5.8S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific_host="muskmelon"
db_xref="ATCC:28858"
                                 country="Spain"
                                             /specific_host="muskmelon"
/db_xref="taxon:61369"
                                                                                     /strain="Fom 28"
                                                                                                 organism="Fusarium oxysporum/mol_type="genomic DNA"
                                                                                                                                                    ocation/Qualifiers
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Pred. No. 27;
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RESULT 48
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 18;
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                                                                                                                                                                                                                                                                                                                                         Submitted (29-JUL-2003) Biotechnology, (Murcia) 30150, Spain
                                                                                                                                                                                                                                                                                                                                                                      Cifuentes, D.
Direct Submission
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Cifuentes,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari
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                Similarity
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Conservative
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176. .333
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29. .175
                                                                                   /product="internal transcribed
                                                                                                                                                                                                               /note≃"forma:
                                                                                                                                                                                                                                         /specific_host="watermelon"
/db_xref="taxon:120297"
                                                                                                                                                                                                                                                                     organism="Fusarium oxysporum"
|mol_type="genomic_DNA"
|strain="Fon_1"
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                                                                      /product="28S ribosomal RNA"
                                                                                                                            product="5.8S
                                                                                                                                                                                 product="18S ribosomal RNA"
                                                                                                                                                                                                                            country="Spain"
                                                                                                                                                        product="internal transcribed
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             100.0%;
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                 Score 18; DB Pred. No. 27;
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                                                                                                                                                        spacer
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  Indels
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  Gaps
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CGTTAATTCGCGTTCCTC 18

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RESULT 49
AY354397
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Pusarium oxysporum f. niveum strain Fon 7 188 ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.88 ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28 ribosomal RNA gene, partial sequence.
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1 (bases 1 to 501)
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Fusarium oxysporum f. Fusarium oxysporum f.
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/mol_type="genomic DNA"
/strain="Fon 7"
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/db_xref="taxon:120297"
/country="Spain"
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 501)
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Pusarium oxysporum f. sp. luffae
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
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AY354399.1 GI:34559404
                               Submitted (29-JUL-2003) Biotechnology, IMIDA,
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/strain="ATCC_18143"
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/db_xref="taxon:120295"
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AF069310
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2 (bases 1 to 506)
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                                                                                                                                                                                                                                                                                         Submitted (31-MAY-1998) Lab. of Plant Physiology and Molecular
Biology, Dept. of Biology, Univ. of Turku, Turku 20014, Finland
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="ATCC 28860"
                                                                              /product="5.8S ribosomal RNA"
297. .446
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b_xref="taxon:243110"
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                 product="28S ribosomal RNA"
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                                                                                                                            note="ITS1"
                                                                                                                                               product="internal"
                                                                                                                                                                             'country="Finland:Espoo"
'note="isolated from barley root in 1986"
                                                                                                                                                                                                            db_xref="taxon:5507"
                                                                                                                                                                                                                             strain="93138"
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Fusarium wilt of cotton: Molecular approaches towards durable disease resistance in Gosspium hirsutum L
Thesis (2002) The University of Sydney, School of Biological Sciences, Macleay Building Al2, Sydney, NSW, Australia, In pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

1 (bases 1 to 506)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Becerra-Lopez Lavalle, L.A., Saleeba, J.A. and Lyon, B.R. Molecular identification and classification of fungi is stem tissue of cotton (Gossypium hirsutum L)
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/product="28S ribosomal RNA"
                                                                                                                                                                                                                                                                                            specific_host="Gossypium hirsutum"
db_xref="taxon:5507"
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'isolate="40-1"
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Fusarium wilt of cotton: Molecular approaches towards durable disease resistance in Gossypium hirsutum L
Thesis (2002) The University of Sydney, School of Biological Sciences, Macleay Building Al2, Sydney, NSW, Australia, In pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Pusarium oxysporum complex.

1 (bases 1 to 506)
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/mol_type="genomic DNA"
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Fusarium wilt of cotton: Molecular approaches towards durable disease resistance in Gosspium hirsutum L
Thesis (2002) The University of Sydney, School of Biological Sciences, Macleay Building Al2, Sydney, NSW, Australia, In pro
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                                                                                                                                                                                                                                                                                                                                                                   AY555719 S15 bp DNA linear PLN 20-MAl Pusarium oxysporum strain F35 185 ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.85 ribosomal RNA gand internal transcribed spacer 2, complete sequence; and 285 ribosomal RNA gene, partial sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Becerra-Lopez Lavalle, L.A., Saleeba, J.A. Direct Submission
                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

1 (bases 1 to 515)

Li,C.-T., Wang,Q.-J., Mo,E.-K., Xu,B.-J., Fang,Z.-M. and Sung,C.-I Taxol production by endophytes isolated from yew tree, Taxus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSW 2006,
           Submitted (24-FEB-2004) Antioxidants Research Lab, Kor Institute of Bioscience and Biotechnology, Yusung-Gu, Chungnam 305-333, South Korea Location/Qualifiers
                                                                                  Direct Submission
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ilarity 100.0%;
Conservative (
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/mol_type="genomic I
/isolate="49-2"
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db_xref="taxon:5507"
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             misc_RNA
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O'Donnell,K., Cigelnik,E. and Nire
Molecular systematics and phylogec
fujikuroi species complex
Mycologia 90 (3), 465-493 (1998)
4 (bases 1 to 520)
O'Donnell,K, and Cigelnik,E.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

1 (bases 1 to 520)
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                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 520)
O'Donnell, K., Cigelnik, E. and Casper, H.H.
Molecular phylogenetic, morphological, and mycotoxin data support
reidentification of the Quorn mycoprotein fungus as Fusarium
                                                                                                                                                                                                                                                                                                                                                                                                            O'Donnell, K. and Cigelnik, E.

Two divergent intragenomic rDNA ITS2 types within lineage of the fungus Fusarium are nonorthologous Mol. Phylogenet. Evol. 7 (1), 103-116 (1997)
                                                                                                 Submitted (21-AUG-1995) Kerry O'Donnell,
University St., Peoria, IL 61604, USA
Location/Qualifiers
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483. .>515
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333. .482
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175. .332
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/mol_type="genomic I
/strain="F35"
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/db_xref="taxon:5507"
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                                         organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/strain="NRRL 22902"
/product="internal transcribed spacer"
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                             _xref="taxon:5507"
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of the Gibberella
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AF502841
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AF176656
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Fusarium oxysporum
Eusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium oxysporum complex.

1 (bases 1 to 521)
Grunden, E., Chen, W. and Crane, J.L.
Grunden, E., Chen, W. and Crane, J.L.
                                            leaf litter ascomycete strain its330
leaf litter ascomycete strain its330
Eukaryota, Fungi, Ascomycota.
1 (bases 1 to 523)
Gilbert, G.S., Garbelotto, M., Chapela,
                                                                                                                                                                                       AF502841 523 bp DNA linear PLN 13-NAY-2-leaf litter ascomycete strain its30 isolate 1000501231 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial
                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grunden,E., Chen,W. and Crane,J.L. Direct Submission Submitted (10-AUG-1999) Center for Biodiversity, Illinois Natural History Survey, 607 E. Peabody Dr., Champaign, IL 61820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fungi Colonizing Microsclerotia Unpublished
Biogeography
Unpublished
                                                                                                                                                            sequence.
AF502841
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                             Dreyfuss, M.M.
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larity 100.0%;
Conservative (
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spacer 1, 5.8S ribosomal RNA,
2, and 28S ribosomal RNA"
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/mol_type="genomic DNA"
/db_xref="taxon:5507"
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                                                Garbelotto, M., Chapela, I.,
                  leaf litter fungi
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-APR-2002) Environmental Studies, Univ
California, Santa Cruz, 1156 High St., Santa Cruz,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusarium oxysporum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                         Fusarium oxysporum complex.

1 (bases 1 to 531)

Gomez-Leyva,J.F., Ochoa-Sanchez,J.C., Loera-Quezada,M.,

Gomez-Leyva,J.F., Ochoa-Sanchez,J.C., Rodriguez-Garay,B.

Leal-Klevezas,D.S., Abeyrathne,P., Nazar,R.N., Rodriguez-Garay,B.

and Martinez-Soriano,J.P.

Sensitive and specific PCR assay to detect the causal agent of th
                                                                                                                                                                                                                         Submitted (08-MAR-2000) Biotecnologia y Bioquimica, Unidad de
Biotecnologia e Ingenieria Genetica de Plantas, CINVESTAV-IPN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusarium oxysporum
                                                                                                                                                                                       Mexico
                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                         Gomez-Leyva, J.F., Ochoa-Sanchez, J.C., Martinez-Soriano, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusarium oxysporum
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                                                                                                                                                                                                                                                                                                                                            Agave tequilana root rot
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164. .318
                /product="18S ribosomal RNA" 27. .174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="leaf litter ascomycete strain its330"
|mol_type="genomic DNA"
                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product="5.8S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'specific_host="Mammea americana"
'db_xref="taxon:194113"
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                                                                                                 /organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="MMaVH13"
                                                            /specific_host="Agave tequilana/db_xref="taxon:5507"
/product="internal transcribed spacer 1"
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Garbelotto,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waalwijk,C., de Koning,J.R.A., Baayen,R.P. and Gams,W.
Discordant groupings of Fusarium spp. from sections Elegans,
Liseola and Dlaminia a based on ribosomal ITS1 and ITS2 sequ-
Mycologia 88, 361-368 (1996)
2 (bases 1 to 544)
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18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S
5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed internal transcribed spacer 2; ITS1; ITS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (08-DEC-1995) C. Waalwijk, Research Inst. for Pl
Submitted (08-DEC-1995) G. Wageningen, NETHERLANDS
Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS
On Jun 15, 2001 this sequence version replaced gi:1103570.
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Hypocreomycetidae, Hypocreales, mitosporic Hypocreales, Fusari
Fusarium oxysporum complex.
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                                                                                                                                                                                                                                                                                                                                                          /organism="Fusarium
/mol_type="genomic I
/strain="F101"
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                            gene="18S rRNA"
                                                                                                                                                                                                                                                                                            gene="18S rRNA"
                                                                                                                                                                                                                                                                                                                          specific_host="carnation"/db_xref="taxon:5507"
               /product="28S ribosomal RNA"
                                                                                                                 336. .486
                                                                                                                                                                                                                                            'product="18S ribosomal RNA"
                              gene="28S rRNA"
                                                                gene="28S rRNA"
                                                                                             note="internal
                                                                                                                           product="5.8 ribosomal
                                                                                                                                              gene="5.8 rRNA"
                                                                                                                                                                            gene="5.8 rRNA"
                                                                                                                                                                                                              note="internal transcribed spacer 1, ITS1"
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1 (bases 1 to 545)

Moricca, S., Kasuqa, T., Mitchelson, K.R. and Ragazzi, A. Moricca, S. Kasuqa, T., Mitchelson, K.R. and Ragazzi, A. Mitchelson, Mitchelson, K.R. and Ragazzi, A. Mitchelson, Mitchelson, K.R. and Ragazzi, A. Mitchelson, Mitchel
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5.85 ribosomal RNA; 5.85 rRNA gene.
Fusarium oxysporum
Fusarium oxysporum
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 546)
Moricca, S., Kasuga, T., Mitchelson, K.R. and Ragazzi, A.
The sequence of the fusarium oxysporum f.s.p. vasinfectum 5.85 rRi
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Submitted (21-MAR-1994) K.R. Mitchelson,
Cell Biology, University of Aberdeen, Abe
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusarium oxysporum Fusarium oxysporum
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                                                                                                                                                                                                     F.oxysporum (f.sp.vasinfectum, X78259
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                                                                                                                                                                                   X78259.1 GI:467738
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/product="5.8S ribosomal RNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sub_species="f.sp.vasinfectum"
db_xref="taxon:5507"
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strain="BIE"
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5.8S ribosomal RNA;
Fusarium oxysporum
Fusarium oxysporum
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Fungal Genet. Newsl. 42, 53-55 (1995)
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/product="5.8S ribosomal RNA"
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strain="Bul"
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/mol_type="genomic DNA"
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                             gene="5.8S rRNA"
product="5.8S ril
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                                                                                                                               'lab host="Gossypium"
'note="host from Cuanza
                                                                                                                                                                                                                                                   mol_type="genomic DNA"
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clone lib="S.Moricca"
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                                                                                                                                                                  tissue type="Mycelium"
clone_lib="S.Moricca"
                                                                                                                                                                                                              sub_species="f.sp.vasinfectum"
db_xref="taxon:5507"
                                                                                                                                                                                                                                                                                         organism="Fusarium oxysporum"
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Pred. No.
                                 ribosomal
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; rusarium oxysporum complex.

1 (bases 1 to 546)

Moricca, S., Kasuga, T., Mitchelson, K.R. and Ragazzi, A.
The sequence of the fusarium oxysporum f.s.p. vasinfectum 5.8S rRN and adjacent ITS 1 and ITS 2 regions Fungal Genet. Newsl. 42, 53-55 (1995)
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                                                                                                                                                                                                                                             Submitted (21-MAR-1994) K.R. Mitchelson, Depart
Submitted (21-MAR-1994) K.R. Mitchelson, Depart
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Norte, Italy"
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e) 5.8S
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Best Local
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AN147369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics and Evolutionary Biology of Fusarium culmorum Thesis (2002) The University of Reading, Whiteknights, Reading, Berkshire, United Kingdom 2 (bases 1 to 552)
Mishra, P.K., Fox.R.T. and Culham, A. Mishra, P.K., Fox.R.T. and Culham, Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarii Fusarium oxysporum complex.

1. (bases 1 to 552)
                                                                     AY462580 552 bp DNA linear PLN 06-DBC-2 gene, partial sequence; internal transcribed spacer 1, 5.85 ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 285 ribosomal RNA gene, apartial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                            18;
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Fusarium oxysporum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-SEP-2002) School of Plant Sciences, Reading, Whiteknights, Reading, Berkshire RG6 6AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mishra, P.K., Fox, R.T.V. and Culham, A.
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  Fusarium oxysporum f. sp.
                                                 AY462580.1 GI:38569372
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                                                                                                                                                                                                                                                                                                              CGTTAATTCGCGTTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/db_xref="taxon:5507"
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
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Wilson Road, East Lansing, MI
Location/Qualifiers
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Catal, M. and Schilder, A.M.C.
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                                                                                                                                                                                                                       Catal,M. and Schilder,A.M.C. A PCR-based method to distinguish Eutypa lata and Eutypella vitis
                                                                                                                                                                                                                                                                                                  Fusarium oxysporum f. sp. vasinfectum
Fusarium oxysporum f. sp. vasinfectum
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
                                                        Submitted (11-NOV-2003) Plant
Wilson Road, East Lansing, MI
Location/Qualifiers
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                                                                                                                                                                              from grapevine 
Unpublished
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                                                                                                                          Direct Submission
                                                                                                                                         Catal, M. and Schilder, A.M.C.
                                                                                                                                                                                                                                                                                  Fusarium oxysporum complex.
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/mol_type="genomic DNA"
/isoTate="PA3"
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/db_xref="taxon:61374"
/organism="Fusarium oxysporum f.
/mol_type="genomic DNA"
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100.0%; Pred. No. 27;
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48823, USA
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616 bp DNA linear PLN 13-DEC-2000 Fusarium oxysporum f. sp. vasinfectum strain Ag149 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

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Comparsion of ribosomal RNA gene sequences between a hete
and two segregants of Fusarium oxysporum f.sp.vasinfectum
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Pusarium oxysporum f. sp. vasinfectum
Pusarium oxysporum f. sp. vasinfectum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
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/db_xref="taxon:61374"
/country="USA: PA"
                                                              /product="5.8S ribosomal RNA"
409. .558
                                                                                               /product="internal transcribed
251. .408
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511. .>555
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361. .510
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Fusarium oxysporum f. sp. vasinfectum
Fusarium oxysporum f. sp. vasinfectum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
AF322076 616 bp DNA linear PLN 13-DEN Fusarium oxysporum f. sp. vasinfectum strain Ag149-III 18S ribosomal RNA gene, partial sequence; internal transcribed sp. 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence AF322076.1 GI:11692814
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Comparsion of ribosomal RNA gene sequences between a heterokaryon and two segregants of Fusarium oxysporum f.sp.vasinfectum
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Comparsion of ribosomal RNA gene sequences between a heterokaryon
Comparsion of Fisarium oxysporum f.sp.vasinfectum
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Fusarium oxysporum f. sp. vasinfectum
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
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                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

1 (bases 1 to 636)

Quader, M. and Riley, I.T.
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1 (bases 1 to 616)
                                                                                             Direct Submission
Submitted (06-NOV-2001) Applied and Molecular Ecology, Adelaide
Submitted (06-NOV-2001) Applied and Molecular Ecology, Adelaide
University, Waite Campus, Glen Osmond, Adelaide, SA 5064, Australia
Location/Qualifiers
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Fusarium oxysporum
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/mol type="genomic DNA"
/strain="Ag149-III"
/db_xref="taxon:61374"
/note="nuclear type segregant
forma_specialis: vasinfectum"
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                                                        /organism="Fusarium oxysporum"
/mol_type="genomic DNA"
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                                     _xref="taxon:5507"
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AY669120
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Direct Submission
Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy
Agriculture Sciences, Wisi Road 247, Fuzhou, Fujian 350003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cao,Y., Lin,Y., Ge,C., Xiao,R. and Liu,B. Comparison of ribosomal RNA gene sequences
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AY667489 DNA linear PLN 20-JUL
Fusarium oxysporum isolate 12-152 internal transcribed spacer
partial sequence; 5.88 ribosomal RNA gene, complete sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /specific_host="Cucumis melo L."
/db_xref="taxon:5507"
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/strain="F-T.1.7-030520"
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Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;

Pusarium oxysporum complex.

1 (bases 1 to 671)

1 (bases 1 to 671)

1 (bases 1 to 671)
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                                                                                                                                                                                                              Cao,Y., Lin,Y., Ge,C., Xiao,R. and Liu,B. Comparison of ribosomal RNA gene sequences among Fusarium oxysporum from different hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
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                                                                                                                            Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy Agriculture Sciences, Wusi Road 247, Fuzhou, Fujian 350003, (
                                                                                                                                                         Cao, Y., Lin, Y., G
Direct Submission
                                                                                                                                                                                               Unpublished
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/db_xref="taxon:5507"
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/mol_type="genomic DNA"
/isolate="12-152"
                                                                   /organism="Fusarium oxysporum"
/mol_type="genomic DNA"
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         /specific_host="Pisum sativum L."
/db_xref="taxon:5507"
/country="China: Fujian, Zhangzhov
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/strain="F-W.6.2-030304"
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AY669125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                               l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-JUN-2004) Biotechnology Center, Agriculture Sciences, Wusi Road 247, Fuzhou, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 678)
Cao, Y., Lin, Y., Ge,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cao,Y., Lin,Y., Ge,C., Xiao,R. and Liu,B. Comparison of ribosomal RNA gene sequences among Fusarium oxysporum from different hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
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CGTTAATTCGCGTTCCTC
                              CGTTAATTCGCGTTCCTC 18
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187. .325
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                                                                                                                                                                                                                                                              /product="18S ribosomal RNA"
188. .326
                                                                                                                                                                                                                                                                                                                                                              /organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/strain="F-X.1.7-030520-12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="internal transcribed
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                                                                                                                                                                                                                                                                                                                             'specific host="Citrullus lanatus (Thunb) Mansfeld"
'db_xref="taxon:5507"
                                                                                                                                              'product="28S ribosomal RNA
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AY188919
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Pusarium oxysporum f. sp. melonis 18S ribosomal RNA gene, part sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1134)
Hatsch,D., Phalip,V. and Jeltsch,J.M.
Hatsch,D., Phalip,V. and Jeltsch,J.M.
Study of the genes encoding cellobiohydrolase-C and topoisomerase
II as target for phylogenetic analysis and identification of
Fusarium at a species level
                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-NOV-2002) Laboratoire de Phytopathologie,
IFR 85 - ESBS -ULP, Boulevard Sebastien Brant,
Illkirch-Graffenstaden, Alsace 67400, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1134)
Hatsch,D., Phalip,V. and Jeltsch,J.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusarium oxysporum f. sp. melonis
Fusarium oxysporum f. sp. melonis
Fusarium oxysporum f. sp. melonis
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
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                                                                                                                                                                                                                  F.oxysporum 5.8S rRNA,
Y07991
 Ballesta, J.P.G.
Direct Submission
                                                                                                               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
                                                                                                                                                Fusarium oxysporum
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26S ribosomal RNA; 5.8S ribosomal RNA; ITS2
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                                                 Iglesias,M.
Unpublished
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475. .>1134
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                                                                  Ballesta, J.P.G.
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Pred. No. 27;
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ITS2,
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and
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Job time : 1413 secs
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Direct Submission
Submitted (20-JAN-1997) J.P.G. Ballesta, Universidad Autonoma
Submitted (20-JAN-1997) M.P.G. Ballesta, Canto Blanco, Madrid, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-SEP-1996) J.P.G. Ballesta, Universidad Autonoma De
Madrid, Centro De Biologia Molecular, Canto Blanco,, Madrid, 28049,
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3 (bases 1 to 1471)
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                                                                                                                                         Similarity
                                                                                                                          Conservative
                                                                                                                                                                                                 /product="hypothetical protein"
/protein_id="CAA69270.1"
/db_xref="GI:1805770"
/db_xref="TIEMBL:P78651"
/ta_nslation="HSHONRRCHLIEIVQPEMQPYRAGIQFRSRRNRHSKKSLPIYVD
ICLGQISKLHVHLRTPTPPVRXSQLSLASKTPKTVLEAESQSEYLYRRIRRHQSSSPE
SILGALKSLAKGTKAIMHENVLLRAELREVREANEILSRR"
                                                                                                                                                                                                                                                                                                                                 /gene="26S rRNA"
/product="26S ribosomal RNA"
<1043. .>1471
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/mol_type="genomic DNA"
/db_xref="taxon:5507"
                                                                                                                                                                                                                                                                                                                                                                                               gene="26S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                            'note="intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="5.8S rRNA"
/product="5.8S ribosomal RNA"
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27;
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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 N_Geneseq_23Sep04:*
1: geneseqn1990s:*
2: geneseqn1990s:*
3: geneseqn2001as:*
4: geneseqn2001as:*
5: geneseqn2002as:*
7: geneseqn2002bs:*
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18
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 21	20	c 19	18	17	16	c 15	14	c 13	12	11	10	9			G G	O U	4.	ი ა	N	_	Result No.
14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	15	15	15	15	15	15	15	15	15.4	15.4	18	9.1	Score
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2457	1231	1231	1200	755	650	554	554	207	9212	9212	1467	615	250	250	128	127	538	538	382	18	Query Match Length
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ADH85065	ABQ28090	ABQ28091	ABL12625	ACF65787	AAS05503	ABQ14483	ABQ14482	ADC92275	ABS99066	AAX13271	ACA18462	ADH82429	ACA12661	AAS47978	AAS48419	ACA13108	ABQ37054	ABQ37055	AAA72783	AAV83697	ID
Adh85065 Enterococ	Abq28090 Oligonucl	Abq28091 Oligonuci	Abl12625 Drosophil	Acf65787 Photornab	Aas05503 Mammalian	Abq14483 Oligonucl	Abq14482 Oligonucl	Adc92275 E. faeciu	Abs99066 Enterococ				Aca12661 Prokaryot			Acal3108 Prokaryot	Abq37054 Oligonucl			Aav83697 Species-s	Description

XFFFF

New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Pusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothrix species.

发문장	P A	PA	E R R	Y P S	\$8\$	Y PR	X P P P P	88 X	X Z Z Z Z Z Z Z Z Z		4 5 5	X A	RESULT : AAV8369' ID AAV		იი		O			ი		Ω		n	a		O		იი	
WPI;	Mor	(us	02-	01-	12-	W09	mod	Syn	Int A. M. M. R. Cun	Spe	26-1	AAV	ЛТ 1 33697 AAV	-535	4 4 5	. 43	42	4 4	39	ω ·	ມ ເປ 7 0	ω (5	ω u 4 u	32	30	2 6	276	2 2	23	22
199	Morrison CJ,	(USSH) US	02-MAY-1997	01-MAY-1998	12-NOV-1998	WO9850584-1	Key modified_base	Synthetic. Fusarium o	Internal transo A. terreus; A. M. racemosus; M. M. circinilloid R. circinans; R Cunninghamella Penicillium not	Species-specif	-FEB-1999	AAV83697;	T 1 697 AAV83697 st		14.4 14.4	14.4		14.4		Α.	14.4	44	14.4	. 4.		44		4.	14.8 14.8	
03473		DEPT	•-	•	٠	A2.	as e	c. oxysporum.	A. nio A. nio 18; M. l lloides 18; R. ella el	cific	æ		standard;		80.0	•			•	80.0		•			•		82.2	•	• •	•
7/03.	Reiss E,	HEALTH	97US-0045400P	98WO-US008926			Location 1 /*tag= /note= '	rum.	ibed spidulans plumbe s f. ci stolon legans; tum; Sp	probe	irst entr		cd; DNA;		110000						-						10587			
	Aido	W HUN	54001)8926			ion/Quali = a = "labell		Fus; Name of the Page of the P	targeted	۲۷)		188														10.			
	Aidorevich L, Choi JS;	HUMAN SERVICES.	•				n/Qualifiers a "labelled with digoxigenin"		(TS2; probe; Aspergim solani; F. monilladicus; A. fumigatus dides; Rhizopus oryzz lzomucor pusillus; lesheria boydii; Sceschenkii; filamento	ted to the internal transc			8P.	ALIGNMENTS	ABQ67197_01	AAD57200	AAD57212	ABL28982	ABN91904 AAH54455	AAH53833	ABO34054	ACH74399	ABQ18323	ABK79312	ACF65387_5	ACF67367_53	ACF72118	ABL02050	AAS52883 ABL12624	29
									Illus flavus; A. niger; forme; Mucor rouxii; ;; e; microsporus; he; R. microsporus; bsidia corymbifera; dosporium apiospermum; bus fungus; ss.	nscribed spacer 2.	-				Continuation (2 of	Continuation (3 of	Aad57212 Petunia R	Abl28982 Drosophil	Abh54455 S. epider	Aah53833 S. epider	Abd34054 Oligonucl	Ach74399 Human gen	Abq18323 Oligonucl	Abk79312 Bacillus	Continuation (6 of Abz26380 Candida e	Continuation (54 o	Acf72118 Photorhab	Abl02050 Drosophil	Abl12624 Drosophil	Aca32983 Prokaryot

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RESULT 2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ITS2) region of various filamentous fungi (see AAV70845-73). The probes are species-specific, and can be used for identifying a species selected from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans, Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus, M. indicus, M. circinilloides f. circinelloides, Rhizopus oryzae, R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallischeria boydii (teleomorph of Scedosporium apiospormum), Penicillium notatum, or Sporothrix schenkii. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi
           an indication of Alternaria contamination. Fungi from the genus Alternaria are ubiquitous saprophytes and are economically important pathogens affecting a wide range of plants. Alternaria are the causative agents of black or brown spot disease in many fruits, vegetables and field crops. The method is used for the detection of Alternaria contamination in food products. The present sequence represents the
                                                                                                         The invention relates to a nucleic acid based method for the detection of Alternaria contamination in a food product. The method involves obtaining and analysing a food product sample for a nucleic acid sequence unique to Alternaria. Detectable levels of the nucleic acid sequence can be used as
                                                                                                                                                                                                                      Nucleic acid based assay and kit for detection of Alternaria contamination in food products involves analyzing the sample product for nucleic acid sequences unique to Alternaria.
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                                                                                                                                                                                                                                                                                                                     Kashi Y,
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(KASH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA72783;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spot disease; brown spot disease; fungi; fruit vegetable;
crop; Alternaria; 5.8s rRNA; detection; ds.
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18; Conserv
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C;
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gene,
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 used in examples illustrating the
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RESULT 3
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ID ABQ37055
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                                      particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the
                                                                                                                               This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CyG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc.
                                                                                                                                                                                                                                                                                                                                                                                  Determining the degree of cytosine diagnosis and prognosis, comprises from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drug; side effect; cancer; central ner
gastrointestinal; respiratory system;
SNP; cell differentiation; ds.
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                                                                                                                                                                                                                                                                                                                                                    Claim 12; 56pp + Sequence Listing; 56pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olek A,
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05-SEP-2000;
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Pred. No.
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em; single nucleotide polymorphi
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Sequence 538 BP;

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Query Match
Best Local Similarity
85.6%;
94.1%;
Score 15.4; DB 6;
Pred. No. 2.1e+02;
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BP; 61

A

61 C;

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256 T; 0 U; 0 Other;

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                                                                                This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-CpC-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of coligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central corrous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation contents of many C residues to be determined simultaneously. AB013410-
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide for detecting cytosine methylation SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABQ37054 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-2002
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05-SEP-2000; 2000DE-01044543
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                                 ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12;
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                                                                                                                                                                                                                                                                                                                                                                                                               56pp + Sequence Listing; 56pp; German.
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94.1%;
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Pred. No. 2.
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RESULT 5
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                                                             Cc polypeptide or its fragment whose expression is inhibited by the cardial standard of the polypeptide; (3) producing the polypeptide; (6) inhibited by the creative of the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for cc proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway cc required for proliferation, or that inhibits cellular proliferation; (8) cc identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies cor a gene on which the test compound that inhibits gene product lies compound's activity; (11) a culture comprising strains in which the gene cc product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the gene cc identifying an organism. The antisense nucleic acids are useful for identifying an archaevance contains active across the contains active activ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prokaryotic essential gene antisense oligonucleotide #978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-2003
19-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
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identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1) a vector comprising a promoter operably linked to the nucleic acid
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Trawick JD,
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(first entry)
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Carr GJ,
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Forsyth
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Xu HH;
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Query Match
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23-MAY-2000; 2000US-020648P.
26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-025625P.
27-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
             The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new trargets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous
     nucleic
                                                                                                                                                                                                                           Claim 1; SEQ ID NO 996; 511pp; English.
                                                                                                                                                                                                                                                          New polynucleotides for the identification and antibiotics, comprise sequences of antisense n
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     acids which
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Xu HH;
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     are required for
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23-MAY-2000; 2000US-02068448P.
26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-025362SP.
22-DEC-2000; 2000US-025931P.
16-FEB-2001; 2001US-0269308P.
                                              The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of cranings. The process the sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of cranings.
of organisms. The present sequence is an antisense oligonucleotide of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                         New polynucleotides for the identification antibiotics, comprise sequences of antisens
                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 555; 511pp; English.
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Yamamoto RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 A; 31 C;
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100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 G; 33 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                           nucleic
                                                                                                                                                                                                                                                                                                                                         development
ucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                           of.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 8
ACA12661/c
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밁
        CC the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(C (1) a vector comprising a promoter operably linked to the nucleic acid conoding a polypeptide whose expression is inhibited by the antisense comprising the vector; (3) an isolated convergence of the fragment whose expression is inhibited by the collect acid; (4) an antibody capable of specifically binding contisense nucleic acid; (4) an antibody capable of specifically binding contisense nucleic acid; (4) an antibody capable of specifically binding contisense nucleic acid; (4) an antibody capable of specifically binding contisense nucleic acid; (4) an antibody capable of specifically binding contisense or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for contisense of the activity of a gene in an operon required for contisense of the activity of contisense of the activity of a gene in an operon required for contisense of the activity of contisense of the proliferation of the biological contisense of the proliferation of the contisense of the compound that inhibits proliferation of an compound acts; (9) manufacturing an antibiotic; (10) profiling a compound acts; (11) a culture comprising strains in which the gene controlled to the controlled of the compound controlled of the compound controlled of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACA12661 standard; DNA; 250
                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or a for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-OCT-2003
19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACA12661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2002; 2002WO-US009107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; ss;
drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prokaryotic essential gene antisense oligonucleotide #531
                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-)
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Trawick
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 531; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences
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(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prokaryotic essential gene; cell proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
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Carr G
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  or underexpressed;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ore 15; DB 4; Lored. No. 3.3e+02; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haselbeck R, Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 250;
  determining the extent
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Xu HH;
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cc strains; or (13) identifying the target of a compound that inhibits the crolliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for required discovery programs, or for screening homologous nucleic acids required crequired for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the 6213 cantisense sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Cf. standardise OS field)
RESULT 9
ADH82429
ID ADH82429
ID ADH8
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Best Local :
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                                                                                                                                                                                                                                                                                                                                         polypeptide,
treating E. :
                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid comprising a sequence encoding an Enterococcus fecalis polypeptide, useful for preparing a composition for diagnosing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis infection; transcription regulatory element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ADH85834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6617156-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       faecalis polynucleotide #314.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0055778P
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100.0%; F
tive 0;
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Mismatches
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The invention relates to Enterococcus faecalis polynucleotides and polypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector comprising the nucleic acid and a cell comprising the recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Enterococcus faecalis infection. This sequence represents an E. faecalis polynucleotide of the invention.

Disclosure; SEQ ID NO 314; 193pp;

English

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RESULT 10
ACA18462
The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense cc nucleic acid; (2) a host cell containing the vector; (3) an isolated continued control of the first fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent CC which each of the strains is present in a culture or collection of
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                                                                                                                                                                                                                                                                                                                                antisense nucleic acids, useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation to late candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-045171/04
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16-MAY-1997;
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commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome AAXI2938 to AAXI3919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with New isolated Enterococcus faecalis polynucleotides and polypeptides used to develop products for the detection of Enterococcus and for vaccines for prevention or attenuation of Enterococcus infection. 1436-1441; 2084pp; English. use of. ä

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RESULT 12
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                                                                                               The present invention relates to a new computer readable medium with an Enterococcus faecalis nucleotide sequence. The invention is useful to diagnose the presence of E.faecalis in a sample or determining the presence of a specific microbe in a sample. The invention is also useful for modulating the growth or pathogenicity of E.faecalis, in a vaccine to confer resistance to Enterococcal infection, for commercial, therapeutic and industrial purposes, and for fermenting a particular source or to produce a particular metabolite. The invention is useful for detecting E.faecalis using biochip technology. The present nucleic acid sequence represents an Enterococcus faecalis contig DNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO are the format was obtained in electronic format directly from USPTO
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                                                                                                                                                                                                                                                                                                                                                               Computer readable medium having recorded on it a Enterococcus faecalis nucleotide sequence useful for detecting diseases related to Enterococcus
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(DILL/) DILLON P J.
(BARA/) BARASH S.
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                                                                                                                                                                                                                                                                                                                   Page; 119pp; English
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                                                           3045 A; 1564 C;
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100.0%; Pred. No. 3.6e+02;
              83.3%; Score 15;
100.0%; Pred. No.
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                                                                                                                                              sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from B. faecium bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide one of 10 fully defined sequences given in the (or comprising 40 one of 10 fully defined sequences given in the nucleic acids, its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid derived from Enterococcus faecium encoding Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. faecium DNA sequence SEQ ID 1902
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                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
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                                           16;
                                                         Similarity
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CGTTAATTCGCGTTCCTC
                                                                                                                                      disclosed E. faecium nucleic acids
                                         Conservative
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88.9%;
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                                                        Score 14.8; DB 10
Pred. No. 4.3e+02;
                                              Mismatches
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Oligonucleotide for detecting cytosine methylation SEQ ID

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12-JUL-2002

(first entry)

ABQ14483;

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                                                                                                                                                                  CThis invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC grosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the CC degree of hybridisation to both classes is determined from the label on CC the amplicon. From the ratio of labels hybridised to the two classes of coligomers, the degree of methylation is calculated. The method is used: CC in for diagnosis and/or prognosis of side effects of therapeutic drugs CC and of a wide range of diseases, e.g. cancer, disorders of the central CC nervous, cardiovascular, gastrointestinal and respiratory systems etc., CC particularly by detecting mutations or single nucleotide polymorphisms CC (SNP's); and (ii) for differentiation of cell or tissue types and for convestigating cell differentiation. The method allows the methylation CC investigating cell differentiation. The method allows the methylation CC disclosure of the degree of cytosine methylation described in the CC disclosure of the invention
                                                                                     Query Match
Best Local
                                                                     Matches
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05-SEP-2000; 2000DE-01044543.
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gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
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                                                                                                                                          Sequence 554 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-2002
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                               1 CGTTAATTCGCGTTCCTC 18
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                                                                                                                                          76
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RESULT 15 ABQ14483/c ID ABQ144

ABQ14483 standard; DNA; 554 BP

Search completed: December Job time: 231 secs

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                                                                                                                                                            This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC grosine (C) but not methylated C, to uracil, then part of the genomic CDNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, CC of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers and the CC degree of hybridisation to both classes is determined from the label on CC the amplicon. From the ratio of labels hybridised to the two classes of cligomers, the degree of methylation is calculated. The method is used: CC in for diagnosis and/or prognosis of side effects of therapeutic drugs CC and of a wide range of diseases, e.g. cancer, disorders of the central CC nervous, cardiovascular, gastrointestinal and respiratory systems ecc., CC particularly by detecting mutations or single nucleotide polymorphisms CC (SNP's); and (ii) for differentiation of cell or tissue types and for CC investigating cell differentiation. The method allows the methylation CC status of many C residues to be determined simultaneously. ABQ13410-CC disclosure of the invention
                                                                   Matches
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Best Local
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                                                                                                                                 Sequence
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 CGTTAATTCGCGTTTATC
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                                                                                                                                   554 BP;
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2000DE-01044543.
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			.a. u														DB		of qual gis	ttoda toda a	0. 10 45	000000	ng c	3553	Gapext	ç	-50	2004,	using	GenCo (c) 19
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Query Match 100.0%; Score 18; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 0.84; Matches 18; Conservative 0; Mismatches 0; Indels

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RESULT 1 US-09-423-233-50 Sequence 50, A, Patent No. 637 GENERAL INFORM APPLICANT TYPE TITLE OF INVE TITLE OF INVE CURRENT APPLI CURRENT APPLI CURRENT FILIN NUMBER OF SEQ SOFTWARE: PATE SEQ ID NO 50 LENGTH: 18 TYPE: DNA ORGANISM: FU US-09-423-233-50		C 44 5	C 43	0 0 421		39		36	ω ω 4• π		c 32		30.	c 29	28	
SULT 1 -09-423-233-50 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: The GOVERNMENT of the Un TITLE OF INVENTION: Nucleic Acids f TITLE OF INVENTION: Other Filamentc FILE REFERENCE: 03063-0341WP CURRENT APPLICATION NUMBER: US/09/4 CURRENT FILING DATE: 2000-06-27 NUMBER OF SEQ ID NOS: 61 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 50 SEQ ID NO 50 TYPE: DNA ORGANISM: FUBBRIUM OXYSPORUM ORGANISM: FUBBRIUM OXYSPORUM -09-423-233-50		13.4		13.4	13.4	13.4	13.4		13.4	13.6	٠		u		13.8	
3-50 3-50 6372430 6372430 FORMATION: The Government of the Unit INVENTION: Nucleic Acids for INVENTION: Other Filamentous RENCE: 0363-0341MP ppLICATION NUMBER: US/09/423 TLING DATE: 2000-06-27 SEQ ID NOS: 61 Patentin Ver: 2.0 18 18 18 1: Fusarium oxysporum 3-50		74.4	•	74.4	74.4		74.4		74.4		٠	76.7	٥.	76.7	76.7	
tion US/094232: rnment of the I Nucleic Acids Other Filament 63-0341WP NUMBER: US/09, 1: 2000-06-27 S: 61 Ver. 2.0 oxysporum		2967 10144	2430	1411	720	549	350 492	350	341 1	3378	49795	12666	9717	9704	9423	
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£ America as Aspergillus Species a		Sequence 94,		Sequence 116	Sequence 1003,		Sequence 4921,			sequence 1, Ap	- 6	1	<u>_</u>	u '	ō,	
an .		App1	-		App		1, Ap	73		AB AB	Appl		20	Appli	Appli	

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Qy 1 CGTTAATTCGCGTTCCTC 18

RESULT 2
US-09-134-000C-314
; Sequence 314, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 314
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-314

83.3%; Score 15; DB 4; Length 615;
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RESULT 4
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US-09-107-532A-1902/c
                                                                                                                 Matches
                                                                                                                                                Query Match
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1902:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40/489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                 Local
                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...207
SEQUENCE DESCRIPTION: SEQ ID NO: 1902:
                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                               84
                                                                                                               l Similarity
16; Conserv
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                                                                            CGTTAATTCGCGTTCCTC 18
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 207 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTAATTCGCGTTCC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                             DRGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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                                                                                                               Conservative
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                                                                                                                             82.2%;
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                                                                                                          Score 14.8; DB
Pred. No. 56;
0; Mismatches
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US-09-669-751-103

Sequence 103, Application US/09669751

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PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2950
LENGTH: 2457
TYPE: DNA
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US-09-134-000C-2950/c
                           Sequence 3059, Application US/09710279

Patent No. 6703492

GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT FILING DATE: 1090/710,279

CURRENT FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472
SOFTMANDER: BASEOTIONS: 4472
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APPLICANT: Greenspan
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: P-NI
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LENGTH: 650
SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 3059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERCOCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/669,751
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/168,579
PRIOR FILING DATE: 1999-12-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                       963 CGTTAATTCCCGTTCCGC 946
                                                                                                                                                                                                                                                                                                                                                                                                     16;
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                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Methods for Identifying Compounds for
Motion Sickness, Vertigo and Other Disorders Related to
Balance and the Perception of Gravity
                                                                                                                                                                                                                                                                                                                                                                                                                   82.2%;
88.9%;
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Pred. No. 71
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Pred. No. 6
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US-09-134-001C-1367/c
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1367
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                                                            ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: nucleic acid sequence US-09-710-279-3819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-710-279-3819
                                                                                                                                       APPLICANT: KIMMERIY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3819
LENGTH: 2815
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1367, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Douestte-Stamm et al
APPLICANT: Lynn Douestte-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/054,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
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LENGTH: 963
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Best Local
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Patent No. 6703492
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Query Match
Best Local Similarity
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 939
                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09710279
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93.8%;
  80.0%;
93.8%;
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    Score 14.4; DB 4;
Pred. No. 1.2e+02;
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                      Length 2815;
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RESULT 9
US-07-972-791-3/c
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US-07-972-791-7/c
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                                                                                                                          Sequence 7, Application US/07972791
Patent No. 5348857
                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                            Best Local
             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SOWA, Blair A.
APPLICANT: SOWA, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 792026
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Brucella abortus
STRAIN: biovar 1 (S2308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kettelberger, Denise TELECOMMUNICATION INFORMATION: TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear LECULE TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 77027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                              1488 GTTAATTCGCGTTC 1475
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                                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3208 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: 713-850-0909
713-850-0165
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                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                         77.00; Pr
100.0%; Pr
                                                                                                                                                                                                                                                                                             77.8%; Score 14; DB 100.0%; Pred. No. 2e-
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                              DB 1;
. 2e+02;
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STREET: CITY: 1

Houston

Texas

USA

ADDRESSEE:

E: PRAVEL, GAMBRELL, HEWITT, & KRIEGER 1177 West Loop South, 10th Floor

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 713-000
TELEX: 792026
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 3345 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ficht, Thomas A
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA NUMBER OF SEQUENCES: 32
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kettelberger, Denise M. TELECOMMUNICATION INFORMATION: TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                             COUNTRY: US
                                                                             APPLICATION NUMBER: UNFILING DATE: 19921106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Brucel:
STRAIN: biovar 1
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 77027
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                                                                                                                                                                                                                                                                                                        GAMBRELL, HEWITT, & KRIEGER
Loop South, 10th Floor
                                                                                               US/07/972,791
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RESULT 12
US-07-972-791-2/c
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                                                                US-07-972-791-2
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 1921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/07972791 Patent No. 5348857
                                Query Match
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Best Local Similarity
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TELEX: 792026
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                             TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                              MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS. OF BRUCELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
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                Local
                                                                             ORGANISM: Brucella abortus STRAIN: biovar 5
                                                                                                                                                STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                                                                           TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1177 | CITY: Houston
                                                                                                                                                                                                                                                                             TELEPHONE:
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14;
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             Similarity
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             100.0%;
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                                77.8%;
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                  Score 14; Pred. No.
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 Mismatches
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2e+02;
                2e+02;
                                Length 3347;
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Gaps
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GTTAATTCGCGTTC 15

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1488 GTTAATTCGCGTTC 1475

US-07-972-791-8/c

Sequence 8, Application US/07972791 Patent No. 5348857

Patent No.

GENERAL INFORMATION:

APPLICANT:

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                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                              Sequence 6, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: PAtentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/972,791 FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 3347 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
ADDRESSEE: PRAVEL, GAMBRELL, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
STREET: L. STREET: Houston
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TELEFAX: 792026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
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                                                                    ADDRESSEE:
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                                                E: PRAVEL, GAMBRELL, HEWITT, & KRIEGER 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ficht, Thomas A. Sowa, Blair A.
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Job time : 61 secs

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5310649-1/c
;Patent No. 5310649
; Patent The APPLICANT: Ficht, The TITLE OF INVENTION:
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ORIGINAL SOURCE:
ORGANISM: Brucella ovis
US-07-972-791-6
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Search completed: December 8, 2004, 11:09:45
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                                                                                                                                                                                                          SEQ ID NO:1:
                                                                                                               Matches
                                                                                                                            Query Match
Best Local 9
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Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/527,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 3361 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 713-850-09
TELEFAX: 713-850-0165
TELEX: 792026
                                                                                                                                                                                                                          FILING DATE: 22-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                           LENGTH: 3434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                    1503 GTTAATTCGCGTTC 1490
                                                 1692 GTTAATTCGCGTTC 1679
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                                                                   2 GTTAATTCGCGTTC 15
                                                                                                                                Similarity
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                         Thomas A.; Sowa, Blair A.; Adams, Garry L. N: METHOD OF DETECTING SPECIES AND BIOVARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                              100.0%;
                                                                                                                                77.8%; Score 14; DB 6; Length 3434; 100.0%; Pred. No. 2e+02;
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                                                                                                                 Mismatches
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Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                         Score
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Match Length DB
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gn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USO9C_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USO9C_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USONA_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USONA_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USONA_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USOC_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USOD_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USONA_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USONA_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USONA_PUB.seq:*
gn2_6/ptodata/1/pubpna/USONA_PUB.seq:*
gn2_6/ptodata/1/pubpna/USONA_PUB.seq:*
gn2_6/ptodata/1/pubpna/USONA_PUB.seq:*
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             15 US-10-046-955-50
18 US-10-363-345A-23645
18 US-10-363-345A-23646
18 US-10-437-963-93618
10 US-10-437-963-978
10 US-09-815-242-996
10 US-09-815-242-956
11 US-10-282-122A-531
11 US-10-282-122A-532
12 US-09-070-927A-334
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Compugen Ltd.
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Sequence 50, Appl
Sequence 23645, A
Sequence 23646, A
Sequence 936.8, A
Sequence 996, App
Sequence 555, App
Sequence 531, App
Sequence 531, App
Sequence 332, App
Sequence 337, App
Sequence 1371, Ap
Sequence 1371, Ap
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14	14	14	14	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.8			14.8	Δ.	14.8		14.8	14.8	14.8	14.8
77.8	77.8	77.8	77.8	80.0	80.0	80.0						•	80.0				•	80.0	•	80.0	•	82.2	•	•	•	•	•		•	•	82.2	82.2
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US-10-363-345A-23188	US-10-363-345A-23187	US-10-363-345A-15974	US-10-363-345A-15973	US-10-398-221-2058	10	0-341-200-1	US-10-341-200-42	US-10-424-599-116221	US-10-424-599-78398	US-10-369-493-35000	US-10-027-632-266929	0-027-632-	US-10-363-345A-20646	US-10-363-345A-20645	US-10-029-386-7594	US-10-363-345A-4914	US-10-363-345A-4913	US-09-974-300-6603	US-10-085-783A-247	US-10-242-535A-247	US-10-032-585-259	US-10-297-465A-1	US-09-815-242-6520	US-10-282-122A-20853	US-10-425-115-145901	US-10-363-345A-14682	US-10-363-345A-14681	0-425	US-10-255-536-103	-10-437-963-	Ļ	Ÿ
Sequence 23188, A		•		Sequence 2058, Ap	10, Ap	19,	4.2	116		35000,			20646	20645,	7594,		4913,		247,	247,	259	e 1, ,	Sequence 6520, Ap	Sequence 20853, A	145901,	14682	14681,	60210		81762	1074	1073,

ALIGNMENTS

RESULT 1 US-10-046-955-50

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APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aidorevich, Liliana
APPLICANT: Aidorevich, Liliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR PRILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 50
LENGTH: 18
TYPE: DNA
ORGANISM: Pusarium oxysporum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50, Application No.
Query Match 100.0%; Score 18; DB 15; Length 18; Best Local Similarity 100.0%; Pred. No. 6.4; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Di APPLICANT: Control and Prevention
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No. US20030129600A1
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RESULT 4
US-10-437-963-93618/c
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US-10-363-345A-23645
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Sequence 93618, Publication No.
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 23646
LENGTH: 538
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23645, Application US/10363345A Publication No. US20040234960A1 GENERAL INFORMATION:
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LENGTH: 538
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alexander olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Method for determining the degree of methylation of defined TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3 FILE REFERENCE: E01/1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Alexander Olek
APPLICANT: Christian Piej
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: CpG-island No: 23646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Chemically OTHER INFORMATION: CpG-island
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                              Local
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mes 16; Conserv
                                                                                                                                                    2 GTTAATTCGCGTTCCTC 18
                                                                                                                                                                                                              Similarity
                                                                                                                  GTTAATTCGCGTTCGTC 89
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Application US/10437963 US20040123343A1
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94.1%;
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Pred. No. 2.3e+02;
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Pred. No. 2.3e+02;
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                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                              Length 538;
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                                                                                                              PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILLING DATE: 2000-09-06
PRIOR PPLICATION NUMBER: 60/230,347
PRIOR FILLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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LENGTH: 4461
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                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/206,848
PRIOR TILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
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                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
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ORGANISM: Oryza sativa
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APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
                                                           FILING DATE: 2000-12-22
                                                                           FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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16; Conserv
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Zyskind, Jud
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Malone, Cheryl
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ilarity 94.1%;
Conservative
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Pred. No. 2.7e+02;
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; TYPE: DNA ; ORGANISM: Enterococcus faecalis US-10-282-122A-978
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                                                                     US-09-815-242-555/c
                                                                                        RESULT 7
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PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
               Sequence 555, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 978
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                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecalis -09-815-242-996
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CURRENT FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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APPLICANT: Haselbeck, Robert
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les 15; Conservative
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5. US20020061569A1
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100.0%; Pred. No.
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/2191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
                                   FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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LENGTH: 250
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/230,335 FILING DATE: 2000-09-06
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Similarity 100.0%; Pred. No.
15; Conservative 0; Mismatc
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Yamamoto, Ro
Forsyth, R.
Xu, H.
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Zyskind, Judith
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Malone, Cheryl
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Trawick, John
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o. US20040029129A1
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                                                                                                                                                                                                                                                                              Robert
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SEQ ID NO 531
LENGTH: 250
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Best Local Similarity
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APPLICANT:
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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                                                                                                               APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
                                       APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                              APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09
                                                                                                                                                                                               APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                 FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-09-09
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Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto, Robert Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen, Kari
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100.0%; Pred. No.
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. 3.5e+02;
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; ORGANISM: Enterococcus faecalis
US-10-282-122A-6332
                                                                                                                                   ; SEQUENCE DESCRIPTION: SEQ ID NO: 334: US-09-070-927A-334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-09-070-927A-334
                                                         Query Match
Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 334: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      NAME: Kenley K, Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Charles A. Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1027 GTTAATTCGCGTTCC 1041
4989 GTTAATTCGCGTTCC 5003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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                               GTTAATTCGCGTTCC 16
                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                    STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                     ENGTH: 9212 base pairs
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                                                                Conservative
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100.0%;
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Dillon
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                                                                  0;
                                                                              Score 15; DB 9;
; Pred. No. 4.8e+(
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4.1e+02;
                                                                                    4.8e+02;
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APPLICANT: Cao Yahua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION Plante and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 43896

LENGTH: 438

TYPE: """
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; Sequence 1371, Application US/09535459
; Publication No. US20030040615A1
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01153717
US-09-535-459-1371
                                                       RESULT 13
US-10-363-345A-1073
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US-10-424-599-43896
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NUMBER OF SEQ ID NOS: 2170
SOFTWARE: PERL Program
SEQ ID NO 1371
LENGTH: 262
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Sequence 1073, Application US/10363345A Publication No. US20040234960A1 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Suean G.
APPLICANT: Stuve, Laura L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mullahy, Sara J.
APPLICANT: Maughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
FILE REFERENCE: PD-1014 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/535,459
CURRENT FILING DATE: 2000-03-24
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                  297 CGTAAATTCGCGTTCATC 314
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88.9%;
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Pred. No. 4.
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Pred. No. 4.8e+02
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Publication No. GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwei
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OTHER INFORMATION: chemically treated genomic DNA; OTHER INFORMATION: CpG-island No: 1073
US-10-363-345A-1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 1074
LENGTH: 554
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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US-10-363-345A-1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-363-345A-1074/c
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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Matches
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CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 1073
                                                                                                                                                                                  Sequence 81762, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1074, Application US/10363345A Publication No. US20040234960A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Method for determining the degree of methylation of defined TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3 FILE REFERENCE: E01/1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Method for determining the degree of methylation of defined TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG FILE REFERENCE: E01/1227
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CURRENT FILING DATE: 2003-03-03
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                                  APPLICANT:
                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                    l Similarity
16; Conservat
INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                        1 CGTTAATTCGCGTTCCTC 18
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                                                                   Cao, Yon
Wu, Wei
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                                  Barbazuk, Brad
                                                       Boukharov, Andrey
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Pred. No. 4.8e
0; Mismatches
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Pred. No. 4.
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1.8e+02;
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Perfect score:
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Listing first 45 summaries
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        16.4
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Match
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Copyright (c) 1993 - 2004 Compugen Ltd.
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BQ483402
CL460875
CL707833
CL7078823
CL7181278
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BH452985
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AZ35920
CG858920
AZ498171
BH14783
CK7014783
AX440799
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CL707833 OR BBa003
CL708823 OR BBa003
CL718823 OR BBa003
CL7188163 OR BBa003
CL7188163 OR BBa003
CL7288163 OR BBa003
AZ359925 IMO103B02
BH452985 SAL USO27
CG858920 ZMMBBc026
AZ498171 IM0335P13
BH144783 TDGE051TH
CK701447 USDA-FP 4
BZ508556 BONSH38TF
AY440797 Armigeres
AG042918 Pan trog1
AY440799 Armigeres
CG810640 FSAA082TF
CA278228 SCBFSD203
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AA785231 BX965280 AJ502973	BX996957 CR045992 CR180215	AZ991070 AZ991080 CR203507 CB066239	AG081712 CB066245 BM616169	BE557132 BG723264 CK200815 CL729708	BI881942 CB406133 CB406152 CR257810
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ALIGNMENTS

	FEATURES		TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BQ483402/c LOCUS DEFINITION
/db xref="ttaxon:4565" /clone="WHB3508_B09_D18" /tissue_type="Roots" /tissue_type="Roots" /dev stage="Full tillering" /dev stage="Full tillering" /clone_lib="Wheat unstressed root cDNA library" /clone_lib="Wheat unstressed root cDNA library" /clone="Vector: Lambda Uni-ZAP xR, excised phagemid /note="Vector: Lambda Uni-ZAP xR, excised phagemid pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants were grown until full tillering stage and root tissue was were grown until full tillering stage and root tissue was collected at Texas Tech University (Zhang, HT Nguyen Lab). Total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript SK(-) phagemids in the TJ	u H	West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818 Email: oandersn@pw.usda.gov Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: SK primer.	Anderson, O.D., Choo, S., Close, T.J., Crossman, C., Fenton, R.D., Lazo, G.R., Nguyen, H.T., Rausch, C.J., Wilson, C., Woo, J. and Zhang, D. The structure and function of the expressed portion of the wheat genomes - Unstressed root cDNA library Unpublished (2002) Contact: Olin Anderson Contact: Olin Anderson of Agriculture, Agriculture Research Service, Pacific US Department of Agriculture, Agriculture Research Service, Pacific	BQ483402.1 GI:21319338 BQ483402.1 GI:21319338 EST. Triticum aestivum (bread wheat) Triticum aestivum Triticum aestivum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.	667 bp mRNA linear EST 03-JUN-2002 WHE3508_B09_D18ZS Wheat unstressed root cDNA library Triticum aestivum cDNA clone WHE3508_B09_D18, mRNA sequence.

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RESULT 3
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CL707833 685 bp DNA linear GOR_BBa0027F10.r OR_BBa Oryza rufipogon genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D., Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D., Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B., Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A. A high-throughput Arabidopsis reverse genetics system Plant Cell 14 (12), 2985-2994 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CL460875 949 bp SAIL III CO6.v1 SAIL Collection SAIL_111 CO6.v1, genomic survey CL460875 G1:45863780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single contiguous sequences. Class: TDNA tagged.
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ABRC Stock Number CS805419; T-DNA left border flanking sequences
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                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SAIL 111 CO6.v1"
/clone="SAIL 5011 Collection"
/note="T-DNA left border sequences were isolated using modified TAIL-PCR strategy"
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                                                                                                                      Oryza rufipogon

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache

Bukaryota; Wagnoliophyta; Liliopsida; Poales; Poaceae;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 701)

Kim, H., Yu.Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,

Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, 7
Tel: 520 626 9595
Fax: 520 621 1259
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GSS.
                                                                                                                                                                                                                                                                                           3', genomic
CL708823
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OR_BBa0030B15.r OR_BBa Oryza
3', genomic survey sequence.
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BACKWARD: CAC TCA TTA GGC ACC CCA
INSERT Length: 161 Std Error: 0.00
Plate: 0027 row: F column: 10
Seq primer: CAC TCA TTA GGC ACC CCA
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University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
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Oryza rufipogon
Oryza rufipogon
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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CL707833
CL707833.1 GI:50594871
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                                                                                 Contact: Rod A. Wing
                                                                                                 OMAP Project
Unpublished (2004)
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Kudrna,D., Muller,C.,
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/lab_host="DH10B-T1 phage re
/clone_lib="OR_BBa"
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/db_xref="taxon:4529"
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Pred. No.
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                                 Tucson,
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hes 0;
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                                                                                                                                                                                                  Embryophyta; Tracheophyta;
a; Poales; Poaceae;
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,C. and Wing,R.
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CL714278/c
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Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 740)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
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CL714278.1 GI:50601316
GSS.
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OR_BBa0038P08.r OR_BBa Oryza
3', genomic survey sequence.
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University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
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BACKWARD: CAC TCA TTA GGC ACC CCA
INBERT Length: 161 Std Error: 0.00
Plate: 0038 row: P column: 08
Seq primer: CAC TCA TTA GGC ACC CCA
                                                                                                                                                                                                                                                                                                                                               Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2004)
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/tlssue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lb="OR_BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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/mol_type="genomic DNA"
/db_xref="taxon:4529"
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                                                                                          /organism="Oryza rufipogon"
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/db_xref="taxon:4529"
/clone="OR_BBa0038P08"
              /tissue_type="young leaves"
/lab host="DH108-T1 phage resistant"
/clone lib="OR BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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100.0%; Pred. No. 2.9e+02;
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RESULT 6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                   Local
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University of Arizona
Forbes Building Room 303, Tucson, A/
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR PRimers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                           AZ359925 262 bp DNA linear GSS 0.100103B02F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0103B02 F, genomic survey sequence.
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BACKWARD: CAC TCA TTA GGC ACC CCA
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Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R
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                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                               AZ359925.1
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                              Mus musculus (house mouse)
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/Lab_host="DH10B-T1 phage resistant"
/Lab_nost="DR BBa"
/Lotone lib="OR BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII;
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/mol_type="genomic DNA"
/db_xref="taxon:4529"
                                                                                                                                                                                                                                                                                                                                                                                                           clone="OR_BBa0106I12"
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                               214
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                               BH452985
BOHGA60TF BOHG Brassica oleracea
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BH452985.1 GI:17638696
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: B column: 02
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University of Utah Genome Center
University of Utah
                                                                                                                                                                  survey sequence.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PM942nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="UUGC1M0103B02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                           genomic clone BOHGA60, genomic
                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 CGTTAATTCGCGTTTCT
Email: steve_lommel@ncsu.edu
Homology: e-val = 7.0e-022. Description = asparaginyl-tRNA
Homology: e-val = 9.10e-022. Description = asparaginyl-tRNA
synthetase, cytoplasmic (asparagine-tRNA ligase), putative
[Arabidopsis thaliana] gi|20140327|sp|09SSK1|SYN3_ARATH
Asparaginyl-tRNA synthetase, cytoplasmic 3 (Asparagine--tRNA ligase
3) (AsnRS 3) gi|25406088|pir|B96734 hypothetical prote Homology:
e-val = 2.4e-022. Description = putative asparaginyl-tRNA
synthetase [Oryza sativa (japonica cultivar-group)]
gi|14587206|dbj|BAB61140.1| putative asparaginyl-tRNA synthetase
[Oryza sativa (japonica cultivar-group)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamilds; Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                                                                                                  Tobacco Genome Initiative (TGI) Nicotiana benthamiana ESTs Unpublished (2004)
Contact: Dr. Steven A. Lommel
Tobacco Genome Initiative
North Carolina State University
Box 7253, NCSU, Raleigh, NC 27606, USA
                                                                                                                                                                                                                                                                                                                                                                                                   Opperman, C.H., Lommel, S.A., Burke, M., Feulner, G., Carlson, J., George, C., Gove, S., Houfek, T.D., Jefferys, S.R., Kalat, S., King, R., Levin, J., Little, P.C., Lumpkin, A., Ross, T., Salstead, A., Scholl, E.H., Sosinski, B.R., Stephens, P.J. and Zekanis, S.H.
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Unpublished (2001)
Other_GSSs: BOHGA60TR
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 277)
1 (bases 1 to 277)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                   Tel: 9195130006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicotiana benthamiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: sheared ends
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/note="Vector: pHOS1;
genomic DNA inserted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Brassica oleracea"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="TO1000DH3"
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S1 using BstXI linkers"
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Best Local
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG858920
CG858920.1 GI:38431633
GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZMMBBc0267L01f ZMMBBc (EcoRI)
5', genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                               Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                     Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Bharti, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2003)
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quality sequence stop: 367
Location/Qualifiers
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732 445 5735
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Location/Qualifiers
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/clone_Tib="SAL_US N.Bentheme"
/clone="Vector: pBluescript S/K +; Site_1: EcoR1; Site_2:
Xhol; Total RNA isolated from tissue, poly A fraction
isolated on oligo-dT column. mRNA reverse transcribed and
double stranded. Poly A dsRNA ranging in size from
400-4000 bp directionally cloned into EcoR1 and Xhol
restricted into pBluescript. EcoR1 site at the 5' end of
the cDNA and Xhol on the 3' side."
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/cultivar="Berkeley"
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                                                                                                                                                                                                                                                          1. .402
                                                                                                                                                                         /mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
                                                                                            /clone="ZMMBBc0267L01"
//ab_host="E. coli DH10B"
//ab_host="E. coli DH10B"
/clone lib="ZMMBBC (ECORI)"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
                                                                                                                                                                                                                                  organism="Zea mays"
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  Score 15.4; DB 9;
Pred. No. 6.2e+02;
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0335 row: P column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 493.
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1M0335P13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0335P13 F, genomic survey sequence.
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 493)
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                           was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared NA was blunt end-repaired with T4 NA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored NA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of phasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/).
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/mol type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Query Match Best Local Similarity 94.1

85.6%; 94.1%;

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Score 15.4; DB 8; Pred. No. 6.3e+02; 0; Mismatches 1

80

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                                                  USDA-FP_4707 Ridge pineapple sweet orange entire seedling Citrus sinensis cDNA clone RSE33A08 5', mRNA sequence.
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tomato demethylated genomic DNA
Insert Length: 1270 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tomato Demethylated Genomic DNA Sequences Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                /Note="Westor: pBluescript SK(-); Site 1: EcoRI; Site 2: /Note="Westor: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; This library was made from short EcoRI digested fragments of the genome of Lycopersicon esculentum ligated into pBS (SK-). The fragments were cloned into the methylation restrictive E.coli strain JM109 with the purpose of enriching the library for non-methylated DNA fragments. This procedure may enrich the pool of cloned fragments in JM109 cells for sequences representing expressed genes. Average insert size 1.27 kb."
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/dev_stage="12-14 weeks post harvest"
/lab_host="B.coli JM109"
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/cultivar="E6203"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Lycopersicon esculentum"
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                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                 Score 15.4; DB 8; Pred. No. 6.3e+02;
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                                                                                                                                                                                                                                                                                                                    DB 8;
                                                                                                                                                                                                                                                                                                                  Length 499;
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e cTOG30P13,
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BZ508556/c
                                                                                                                                                                                                                                                                                                                                                                   SOURCE
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                         Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other GSSs: BONSHABTR
Contact: Chris Town
                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassicacea; lo 588)

1 (bases 1 to 588)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                             BONSH38TF BO 1.6 2 KB tot Brassica genomic survey sequence.
BZ508556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GTTAATTCGCGTTCCTC 18
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Contact: Michael Bausher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bausher, M., Shatters, R., Chaparro, J., Dang, P., Hunter, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 547)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Citrus sinensis
                                                                                                           9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                   Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                           GSS.
                                                                                                                                                                                                                                                                                                                                                                                     Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                           BZ508556.1 GI:27031477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An expressed sequence tag (EST) set from Citrus sinensis L. Osbeck
                                       Class: sheared ends
                                                       DNA is from a doubled haploid 
Seq primer: TF
                                                                                             Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    investigations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   South Rock Rd., Fort Pierce, (772) 462-5918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (772) 462-5961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="entire seedling"
/dev stage="50 days after germination"
/lab_host="XI1-Blue"
/clone_lib="Ridge pineapple sweet orange entire seedling"
/clone="Vector: pBluescript II SK+; Site_1: EccRI; Site_2:
XhoI, A high quality EST with at least 200 contiguous
bases at Trace Tuner score of 20 or better"
                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cultivar="Ridge Pineapple"
db_xref="taxon:2711"
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Pred. No. 6.3e+02;
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clone BONSH38,
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RESULT 15
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                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 669)

Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Rusch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Kuo, H.-K., Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.

Direct Submission
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Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Armigeres subalbatus
Armigeres subalbatus
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      אמייטידיי 669 bp mRNA linear H. Armigeres subalbatus ASAP ID: 40469 putative: alanine aminotransferase mRNA sequence.
AY440797
                                                                                                                                                                                                                                                                                                                                                                                                            More information about this sequence is available in ASAP (A Systematic Annotation Package for community analysis of genomes) from the University of Wisconsin-Madison at https://apap.ahabs.wisc.edu/annotation/php/logon.php.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-OCT-2003) Animal Health and Biomedical Sciences, University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI 53706, USA
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/note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared total DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BONSH38"
/note="putative: alanine aminotransferase; similar to Anopheles gambiae ENSANGP00000017843 v14.2.1 at Ensembl; ASAP-UW Feature ID: 40469"
                                                                                                                                                                                                                 /organism="Armigeres subalbatus"
/mol_type="mRNA"
/isolation_source="perfused hemolymph of bacteria-innoculated organisms at 1, 3, 6, 12, hours post-innoculation"
/db_xref="taxon:124917"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Brassica oleracea"
                                                                                             cell_type="hemocyte"
/tissue_type="hemolymph"
/dev_stage="adult"
note="ASAP-UW Feature ID: 40468"
                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                  sex="female"
                                                                              . 669
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                                                                                                                                                                                                                                                                           and 24
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32
                  1 CGTTAATTCGCGTTCCT 17
                                             Similarity
CGTTAATTCCCGTTCCT 48
                                   Conservative
                                            85.6%;
94.1%;
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                                             Score 15.4; DB 3; Pred. No. 6.4e+02;
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                  GenEmbl:*

1: gb_ba:*

2: gb htg:*

3: gb_n:*

4: gb_on:*

5: gb_ph:*

6: gb_ph:*

9: gb pl:*

9: gb pl:*

10: gb_ro:*

11: gb sts:*

11: gb sts:*

11: gb sts:*

12: gb_y:*

13: gb_u:*

14: gb wi:*

15: em_bu:*

16: em_fun:*

17: em_hum:*

18: em_on:*

20: em_on:*

21: em_or:*

22: em_or:*

23: em_or:*

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25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_u:*

30: em_htg_hum:*

31: em_htg_lus:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
em_htgo_hum: *
em_htgo_mus: *
em_htgo_other: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS TITLE JOURNAL	RESULT 1 AR206445 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM		44	42 43	41	39 40	38	c 36	35	C 33	··· ພ ເ	30	2 6 2 9	27	ಬ ೧ ೮	214	2 22	21	30 30	18	16	15	13	<u>, , , , , , , , , , , , , , , , , , , </u>	0 0 110		0 7	თ (ፌ ռ	ω		Result No. S
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            AY226096 298 bp DNA linear PLN 27-MAR-2003 Nectria haematococca 5.8s ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28s ribosomal RNA gene, partial sequence.

RNA gene, partial sequence.

AY226096
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Patent: JP 2001525665-A 51 11-DEC-2001;
PATENTE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O
CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND
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Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
1 (bases 1 to 21)
Morrison, C.J., Reiss, E., Aidorevich, L. and Choi, J.S.
Nucleic acids for detecting Aspergillus species and other
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Fusarium solani
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02-MAY-1997 US 60/045400
CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO
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JP 2001525665-A/51
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/db_xref="taxon:169388"
/note="Fusarium solani"
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GI:29293692
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Nucleic acid
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BD083591
BD083591.1 GI:22629201
JP 2001525665-A/6.
Fusarium solani
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Morrison, C.J., Reiss, E., Aidorevich, L. a
Nucleic acids for detecting Aspergillus
filamentous fungi
Patent: US 6372430-A 6 16-APR-2002;
Location/Qualifiers
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Millar, B.C., Xu, J. and Moore, J.E.
Direct Submission
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Nectria haematococca
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Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria
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/mol_type="unassigned DNA"
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IL Patent: JP 2001525665-A 6 11-DEC-2001;
PATENT: JP 2001525665-A 6 11-DEC-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O
CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND
PREVENTION TECHNOLOGY TRANSFER OFFICE
OS FUBBRIUM SOLBNI
PN JP 2001525665-A/6
PD 11-DEC-2001
PF 01-MAY-1998 JP 1998548275
PR 02-MAY-1998 JP 1998548275
PR 02-MAY-1997 US 60/045400
PI CHRISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO
PI CHRISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO
PI CHRISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO
PI CHOI
PC C12Q1/68
CC Topology: Linear;
Location/Qualifiers.
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                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 319)

Choi, J.S., Westerman, J.M. and Morrison, C.J.

Rapid differentiation of filamentous fungi using species-specific
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Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.
Nucleic acids for detecting Aspergillus species and other
                                                                                                                                                                              Choi, J.S., Westerman, J.M. and Morrison, C.J. Direct Submission
                                                                                                                                                                                                                                                                                                                                           Fusarium solani
Fusarium solani
                                                                                                                                                                                                                                                                                                                                                                                                           RNA gene, partial sequence. AF117921
                                                                                                                                                                                                         Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
2 (bases 1 to 319)
                                                                                                                                                                                                                                         DNA probes
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                                                         /organism="Fusarium solani"
|mol_type="genomic DNA"
|db_xref="taxon:169388"
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                  /product="5.8S ribosomal RNA"
160. .272
                                                                                                                            Jocation/Qualifiers
                                                                                                                                                               (09-SEP-1998)
'product="internal transcribed spacer
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db_xref="taxon:169388"
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Pred. No. 10;
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Best Local
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1 CTAACACCTCGCAACTGGAGA 21
              Pusarium solani internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; internal transcribed spacer 2, and 28S ribosomal RNA gene, partial sequence. AP161222
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Submitted (02-OCT-2003) Department of Plant Pathology, Yunnan
Arricultural University, LongTou Street, Kunming, Yunnan 6502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 468)
Wang, Y. Y., Whitehead, M.,
and Zhang, Z.Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang, Y.Y., Whitehead, M., and Zhang, Z.Q.
Genetic analysis of pathe yanilla plantation
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari

1 (bases 1 to 468)
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sequence; 5.8S ribosomal RNA gene, complete
transcribed spacer 2, partial sequence.
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273. .>319
                                                                                                                                                                                                                                                                                                                                                                                      /specific_host="Vanilla planifolia"
/db_xref="taxon:252400"
                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Fusarium sp.
/mol_type="genomic_DNA"
/isolate="ML-2-1"
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/product="28S ribosomal RNA"
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GI:6941832
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AY043472/c
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Submitted (21-JUN-1999) Center for Biodiversity, Illinois Natural Submitted (21-JUN-1999) Center for Biodiversity, Illinois Natural History Survey, IL Dept. Natural Resources, 607 E. Peabody Dr., Champaign. IL 61820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusarium solani
Fusarium solani
Fusarium solani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Fungi; Ascomycotaes; Nectriaceae; Nectria.

Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 471)
Grunden,E., Chen,W. and Crane,J.L.
Fungi Colonizing Microsclerotia of Verticllium dahliae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY043472 471 bp DNA linear Nectria haematococca strain 35 internal transcribed ribosomal RNA gene, and internal transcribed spacer
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Grunden, E., Chen, W. and Crane, J.L.
                                                                                                                                                                             Catol
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                                                                                                                                                                                                                                                                                       Miller,R.N.G. and Lopes,C.A. rDNA sequence variability in Fusarium solani populations associated with eumartii wilt and dry rot of potato in Brazil
                                                                                                                                                                               Submitted (03-JUL-2001) Genomic Biotechnology, Universidade Catolica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,
                                                                                                                                                                                                                 Miller, R.N.G. and Lopes, C.A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                 Fusarium solani
                                                                                                                                                                Brazil
                                                                                                                                                                                                                                                                      Unpublished
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/noTe="anamorph: Fusarium solanii"
complement(1. .471)
/note="contains internal transcribed spacer 1,
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/mol_type="genomic DNA"
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                                                                     /mol_type="genomic DNA"
/strain="35"
                                                                                                                                           Location/Qualifiers
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                                                    db_xref="taxon:169388"
                                                                                                       organism="Fusarium solani"
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d spacer 1, 5.8S
r 2, complete
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471 bp DNA linear Nectria haematococca strain 39 internal transcribed
                                                                                                                                                                                                                              sequence.
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Direct Submission
Submitted (03-JUL-2001) Genomic Biotechnology, Universidade
Catolica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miller,R.N.G. and Lopes,C.A. rDNA sequence variability in Fusarium solani populations with eumartii wilt and dry rot of potato in Brazil
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Fusarium solani
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Hypocreomycetidae; Hypocreales; 1 (bases 1 to 471)
Miller, R. N. G. and Lopes, C. A.
rDNA sequence variability in Fus
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                                                                                  Bukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreomycetidae; Hypocreales; Nectriaceae; I
                                                                                                                               Fusarium solani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /noTe="anamorph: Fusarium solanii" complement(1. 471) /note="contains internal transcribed spacer 1, ribosomal RNA, and internal transcribed spacer
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/strain="39"
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/mol_type="genomic DNA"
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spacer 1, 5.8S
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AP132801
478 bp DNA linear PLN 20-JAN-2000 Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal RNA, and internal transcribed spacer 2, complete sequence.
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Miller,R.N.G. and Lopes,C.A.
Miller,R.N.G. and Lopes,C.A.
Direct Submission
Submitted (03-JUL-2001) Genomic Biotechnology, Universidade
                                                                                                                                                                                                                                                                                                                                                      Submitted (13-OCT-1995) Arti Duggal, Forestry, Univ. of Toronto, Willcocks St., Toronto, Ont. MSS 3B3, Canada
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Nectriaceae; N
1 (bases 1 to 477)
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Direct Submission
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                                                                                           CTAACACCTCGCAACTGGAGA 438
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llarity 100.0%;
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complement(1..47
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307. .477
/note="internal transcribed spacer 2;
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ribosomal RNA, and internal transcribed spacer
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/mol_type="genomic DNA"
/db_xref="taxon:169388"
1. .150
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/mol_type="genomic DNA"
/strain="83"
                                                                                                                                                                                                                                                           note="internal transcribed spacer 1;
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Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

El (bases 1 to 478)

Harrington, T.C., Steimel, J.P., Workneh, F. and Yang, X.B.
Molecular Identification of Fungi Associated with Vascular
Discoloration of Soybean in the North Central United States
Discoloration of Soybean in the North Central United States
L Plant Dis. 84 (1), 83-89 (2000)

El (bases 1 to 478)

Harrington, T.C., Steimel, J.P., Workneh, F. and Yang, X.B.
Direct Submitted (03-MAR-1999) Plant Pathology, Iowa State University,
Room 351 Bessey Hall, Ames, IA 50011, USA
L Cation/Qualifiers
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AF132801.1
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Nectria haematococca

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 478)

Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.

Phylogenetic analysis of phytopathogenic fungus, Fusarium solar

Phylogenetic analysis region

Mycol. Res. 104 (10), 1175-1183 (2000)

2 (bases 1 to 478)
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Nectria haematococca strain K-1 internal transcribed spacer
ribosomal RNA gene, and internal transcribed spacer 2, compl
                                                                                                           University,
                                                                                                                           Submitted (12-MAY-1999) Molecular
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/organism="Nectria haematococca"
/mol_type="genomic DNA"
/strain="K-1"
                                                                                  ocation/Qualifiers
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/note="ITS2"
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isolate="P185"
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db_xref="taxon:169388"
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Search completed: October Job time: 172.543 secs
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Matches 21; Conservative 0; Mismatches
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AFI50460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suga, H., Hasegawa, T., Mitsui, H., Kageyama, K. and Hyakumachi, M. Phylogenetic analysis of phytopathogenic fungus, Fusarium solani based on the rDNA-ITS region
Mycol. Res. 104 (10), 1175-1183 (2000)
2 (Dases I to 478)
3 (Dases I to 478)
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1 (bass 1 to 478)
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Nectria haematococca
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/product="internal transcribed spacer 2"
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note="anamorph: Fusarium solani"
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/mol type="genomic DNA"
/strain="F1"
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/note="anamorph: Fusarium solani"
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23) k	20	19	18	17	16	c 15	14	13	12	11	10	9	8	7	Q	5	4	w	2	–	Result
15.8	15.0	15.8	15.8	15.8	15.8	15.8	16	16	16.2	16.2	16.2	16.2	16.2	16.2	17	17	19	19	19	21	21	Score
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Ada70422 Rice gene			Abl09972 Drosophil	Ab102977 Drosophil	Abl09973 Drosophil			Abq45159 Oligonucl	Ade82432 Human DNA	Adb98063 HBM-relat	Acc45363 Human HBM	Abk22781 Human hig	Aba82622 Human HBM	Add44826 Rat gene		Aac37182 Arabidops	Abv78724 C. sinens	Aav59009 F. avenac	Aaa61893 Fusarium	Aav70850 Internal	Aav83698 Species-s	! !

New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothr

Sporothrix

Example 1; Page 22; 45pp; English

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	,
15.	15.	15.	15.	15.	15.	15.	15.	15.	15.	15.	15.	15.	15.	15.	15.	15.	15.	15.	15.4	15.4	
4.	4	4	4	4	4	4.	4	4	4	4	4	4	4	4	4	4	4	4	4.	4	•
73	73.3	73.3	73	73.3	73	73.3	73	73.3	73	73	73.3	73	73	73	73	73.3	73.3	73	73	73	i
'n	'n	'n	س	<u>.</u>	'n	'n	'n	'n	'n	'n	W	۳.	'n	'n		'n	'n	<u>.</u>	٠ س	'n	
38	36	29	6	4	w	ω	w	N	2	N	N	N	2	N	_	_	_	<u>_</u>	ш		
8494	36181	29555	6325	676	713	3433	061	2853	790	790	2790	787	2310	034	1884	1388	388	1260	1110	989	
ø	9	N	4	4	4.	4	4	4	7	4.	4	7	4	7	4	9	9	4	7	4	×
ADB7427	ADB74371	AAV74517	ABL06620	ABL08318	ABL15001	ABL11644	ABL18502	ABL15238	ACA19827	AAS55168	AAS54538	ACF73619	AAS52105	ABV73338	AAS55358	ADD47423	ADE58528	ABL11645	ACA37427	ABL18503	100000
Adb74275	Adb74371	Aav74517	Ab106620	Ab108318	Abl15001	Abl11644	Abl18502	Abl15238	Aca19827	Aas55168	Aas54538	Acf73619	Aas52105	Abv73338	Aas55358	Add47423	Ade58528	Ab111645	Aca37427	Abl18503	100.00
š	ž	SE	Dr	B	DH	рŗ	멎	밁	Pr	SE	St	SE	38	3	33	Hu	Hu	Dr	Pr	Dr	ç
Mycobacte	Mycobacte	Staphyloc	Drosophi	Drosophi	Drosophi	Drosophi	Drosophi	Drosophi	Prokaryo	Staphyloc	Staphyloc	Staphyloc	Staphyloc	M. sexta	Staphyloc	Human ger	Human ger	Drosophi	Prokaryo	Drosophi	OT COOPIE

ALIGNMENTS

RESULT 1 AAV83698

AAV83698 standard; DNA;

21 ВP

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Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; M. racemosus; M. plumbeus; M. indicus, A. fumigatus; M. dircinalloides f. circinelloides; Rhizopus oryzae; R. microsporus; R. circinals; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
                                                                                                                                                                                                                                                                       modified_base
                                                                                 WPI; 1999-034737/03.
                                                                                                        Morrison
                                                                                                                                                      02-MAY-1997;
                                                                                                                                                                              01-MAY-1998;
                                                                                                                                                                                                      12-NOV-1998.
                                                                                                                                                                                                                              WO9850584-A2.
                                                                                                                                                                                                                                                                                                             Fusarium solani.
                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                  Penicillium notatum; Sporothrix schenkii; filamentous fungus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Species-specific probe targeted to the internal transcribed spacer 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV83698;
                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                     CJ, Reiss E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                      97US-0045400P
                                                                                                                                                                              98WO-US008926
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                   /*tag=  a
/note= "labelled with digoxigenin"
                                                                                                       Aidorevich L, Choi JS;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probes AAV83677-708 are derived from the internal transcribed spacer 2 (ITS2) region of various filamentous fungi (see AAV70845-73). The probes are species-specific, and can be used for identifying a species selected from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans, F. solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus, M. circinans, R. circinelloides, Rhizomucor pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallesheria boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenkii. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi
            The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans, Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus, M. indicus, M. circinilloides f. circinelloides, Rhizopus oryzae, R.
                                                                                                                                                                                                New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothr
                                                                                                                                                  Claim 1; Page 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. ni A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxi A. racemosus; M. plumbeus; M. indicus; A. fumigatus; M. racemosus; M. plumbeus; M. indicus; Rhizopus oryzae; R. microsporus; M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus;
                                                                                                                                                                                     species
                                                                                                                                                                                                                                                                        WPI; 1999-034737/03
                                                                                                                                                                                                                                                                                                       Morrison CJ,
                                                                                                                                                                                                                                                                                                                                                                         02-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9850584-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusarium solani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV70850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21
                                                                                                                                                                                                                                                                                                                                      (USSH ) US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penicillium notatum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV70850 standard; DNA; 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                      DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                     Reiss E,
                                                                                                                                                                                                                                                                                                                                                                        97US-0045400P.
                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US008926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 A;
                                                                                                                                                  45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spacer 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sporothrix schenkii; filamentous fungus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                     Aidorevich L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ITS2) and adjacent regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 U;
                                                                                                                                                                                                                                                                                                     Choi JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 Other;
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                                                                                                                                                                                                   Sporothrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. niger;
rouxii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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stolonifer, Rhizomucor pusillus,

Absidia

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RESULT 3
ADA61893
ADA6189
ADA7189
ADA7
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Best Local &
                           mutants which are potentially useful as screening tools for antiviral compounds. The compounds may also be used to establish or determine the site at which other antivirals bin be to the total transcribed spacer (e.g., by competitive inhibition). The present sequence represents the ribosomal DNA (TDNA) internal transcribed spacer (ITS) region of Fusarium sp. MF6381, which may be used to characterise MF6381. (Updated on 15-SEP-2)
                                                                                                                                                                                                the inhibition of HIV integrase and in the prevention and treatment of HIV infection. A wide range of state of HIV infection may be treated: AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex); both symptomatic and asymptomatic HIV infection; and actual or potentic exposure to HIV. The compounds may be used to isolate HIV integrase
                                                                                                                                                                                                                                                                                                                                             HIV integrase. The invention encompasses cultures of Fusarium sp. MF6381. The invention also relates to a composition comprising a compound of the invention in combination with an AIDS antiviral aggent, an immunomodulator and an antiinfective agent. The compounds of the invention may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 14; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New steroid compounds are HIV integrase inhibitors used for treating HIV infection and AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC HIV integrase inhibitor; steroid compound; human immunodeficency o acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related comple symptomatic infection; asymptomatic infection; potential HIV expos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corymbifera, Cunninghamella elegans, Pseudallesheria boydii (tele of Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenkii. The probes can be used for differentiating filamentous species from each other and from other medically important fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel steroid compounds derived from the African soil fungus Fusarium sp. MF6381 (ATCC 74469) which act as inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-2003
14-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Singh SB, Zink DL,
Dombrowski AW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusarium sp. MF6381 rDNA internal transcribed spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA61893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA61893 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTAACACCTCGCAACTGGAGA 21
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   be used to field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Felock PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 T; 0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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0.77;
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                                 15-SEP-2003
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RESULT 4
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Best Local
                                                                 This sequence represents an internal transcribed spacer (ITS) sequence of the invention. The primer pairs, based on the ITS sequences, are used for the PCR amplification detection of wheat Microdochium and Fusarium fungal pathogens, especially M. nivale, F. graminearum, F. culmorum, F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different strains of fungi show different symptoms during infection, which may or may not be due to infection. Early identification of the strain causing the infection allows early, and more specific fungicidal treatment. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2003
25-MAR-2003
06-JAN-1999
                                                                                                                                                                                                                                                                                                  Beck
                                                                                                                                                                                                                                   Wheat pathogen internal transcribed spacer sequences - used as a basis for primers for the species-specific polymerase chain reaction detection
                                                                                                                                                                                                   Claim 1; Col 29-30; 20pp; English.
                                                                                                                                                                                                                                                                                                                                               04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                     04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                              Sequence 561
                                                                                                                                                                                                                                                                         WPI; 1998-593995/50
                                                                                                                                                                                                                                                                                                                        (NOVS ) NOVARTIS
                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibberella avenacea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen; fungal pathogen identification; infection identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV59009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV59009 standard; DNA; 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                avenaceum
                                                                                                                                                                                                                            the pathogens.
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ch 90.5%; So 19: Similarity 100.0%; I 19; Conservative 0;
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                                              ₿₽;
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(first entry)
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/note=_"ITS1"
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                                              145 A; 152 C; 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 144 C; 118
 ; Score 19; DB
%; Pred. No. 8.6
0; Mismatches
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                                              G; 126 T; 0
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            DB 2;
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8.5;
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                      Length 561;
                                              U; 3 Other;
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Matches 19; Conserv
                                                                                                                     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 659 BP; 183
                                                                                                promoter; termination
                                                                                                                                                                                                                                               17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel base sequence which is part of a fully defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispora. The base sequences can be used for the classification of Cordyceps sinensis. The sequence represents a C. sinensis rRNA sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HEAL-)
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                                                                                                                                                                                               Arabidopsis thaliana DNA fragment SEQ ID NO: 16470
                                                                                                                                                                                                                                                                                                                                             AAC37182 standard; DNA; 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. sinensis rRNA sequence #23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-639075/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JAN-2001; 2001JP-00004805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cordyceps sinensis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV78724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAACACCTCGCAACTGGA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA gene base sequence of Cordyceps sinensis of Cordyceps sinensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; 33pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTAACACCTCGCAACTGGA 491
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                                                                                              sequence; ss.
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EP1033405-A2

Arabidopsis thaliana

06-MAY-1999 11-MAY-1999 12-MAY-1999 12-MAY-1999 12-MAY-1999 13-JUN-1999 10-JUN-1999 10-JUN-1999 11-JUN-1999	25-FEB-2000; 25-FEB-2000; 25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 23-MAR-1999; 23-MAR-1999; 24-APR-1999; 16-APR-1999; 16-APR-1999; 16-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 24-MAY-1999; 30-APR-1999; 30-APR-1999; 30-APR-1999; 30-APR-1999;
99US-0132487P 99US-013428P 99US-0134218P 99US-0134218P 99US-0134219P 99US-013421P 99US-013421P 99US-013421P 99US-013421P 99US-013523P 99US-013522P 99US-013522P 99US-0137528P 99US-0137528P 99US-0137528P 99US-0138647P 99US-0138647P 99US-0139453P 99US-0139453P 99US-0139458P 99US-0140458P 99US-0140548P 99US-0140548P 99US-0140548P 99US-0140548P 99US-0140548P 99US-0140548P 99US-0140548P	2000 0000 0000 0000 0000 0000 0000 000
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99US-0145192P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145918P 99US-0145918P 99US-0145918P 99US-0146388P 99US-0147302P 99US-0147302P 99US-0147302P 99US-0147303P 99US-0147303P 99US-0147303P 99US-0147303P 99US-0147303P 99US-0148319P 99US-01483319P 99US-0148331P 99US-0148331P 99US-0148331P 99US-0149723P 99US-0149723P 99US-0151086P 99US-0151086P 99US-0151088P 99US-0151089P 99US-015373P 99US-015373P 99US-015373P 99US-0154039P 99US-0154039P 99US-0154039P 99US-0154039P	9US-0142051 9US-014239 9US-014280 9US-014292 9US-014354 9US-0144362 9US-0144000 9US-014408 9US-014408 9US-014433 9US-014433 9US-014433 9US-014433 9US-014433 9US-014433 9US-014433 9US-014433

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RESULT 7
AAC45891
AC45891
AC45891
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DT 18-C
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23-SEP-1999
24-SEP-1999
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12-OCT-1999
21-OCT-1999
22-OCT-1999
                                                                                                                                                                                 Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
     25-FEB-1999;
05-MAR-1999;
                                                 25-FEB-2000; 2000EP-00301439.
                                                                                     06-SEP-2000.
                                                                                                                    EP1033405-A2
                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                 Arabidopsis thaliana DNA fragment
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                                                                                                                                                                                                                                                                                                                                                  standard; DNA; 2706
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99US-0155659P

99US-015665P

99US-015753P

99US-0157753P

99US-0157865P

99US-015832P

99US-015823P

99US-015929P

99US-015923P

99US-0159331P

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99US-016938P

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99US-0160814P

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99US-0161406P

99US-0161406P

99US-0161361P

99US-0161361P

99US-0161361P

99US-0161361P

99US-0161393P

99US-0161393P

99US-0161393P

99US-0161393P
   99US-0121825P.
99US-0123180P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                    BP.
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89;
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     09-MAR-1999
25-MAR-1999
25-MAR-1999
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26-APR-1999
16-APR-1999
16-APR-1999
17-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
24-MAY-1999
14-MAY-1999
14-JUN-1999
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30-JUL-1999
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99US-0123548P
99US-0126785P
99US-0126785P
99US-0127462P
99US-013071P
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99US-01418287P
99US-01418297P
99US-0142920P
99US-0143542P
99US-0143542P
99US-0143542P
99US-0143542P
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RESULT 8
ADD44826
ID 44826
AC ADD4
XX ADD7
AC ADD7
CP Rat;
KW Rat;
KW Spin
KW Spin
KW Spax
XX W020
XX W14-A
PR 114-A
PR 
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Best Local S
Matches 17
                                                                                                                                                                         14-AUG-2001;
01-NOV-2001;
26-NOV-2001;
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07-0CT-1999
13-0CT-1999
13-0CT-1999
13-0CT-1999
14-0CT-1999
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spinal se
spared ne
                              Woolf
                                                                                      (GEHO
(FARB
                                                                                                                                                                                                                                                                                          14-AUG-2002; 2002WO-US025765
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                                                                                                                                                                                                                                                                                                                                                                                                            WO2003016475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene Y00311, SEQ ID NO 10257.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s; gene; pain; neuronal tissue; gene therapy;
segmental nerve injury; chronic constriction
nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 CACCTCGCAACTGGAGA 21
|||||||||||||||||
20 CACCTCGCAACTGGAGA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          norvegicus.
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                                                                                      GEN HOSPITAL
BAYER AG.
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Similarity 100.0%; I
17; Conservative 0;
                              D'urso
                                                                                                                                                                         2001US-0312147P.
2001US-0346382P.
2001US-0333347P.
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99US-0158232P

99US-0158369P

99US-0159294P

99US-0159295P

99US-0159331P

99US-0159331P

99US-0159331P

99US-0159637P

99US-0160767P

99US-0160770P

99US-0160768P

99US-0160768P

99US-0160815P

99US-0160815P

99US-0161404P

99US-0161361P

99US-0161361P
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Pred. No. 1e+02;
0; Mismatches
                           Costigan M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCI;
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15-JUL-1999
16-JUL-1999
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119-JUL-1999
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120-JUL-1999
120-JUL-

99US-0144005P 99US-0144086P 99US-0144331P 99US-0144331P 99US-0144331P 99US-0144331P 99US-0144334P 99US-0144884P 99US-0145088P 99US-0145088P 99US-0145088P 99US-014508P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0146386P 99US-0147302P 99US-0147302P 99US-0147303P 99US-0147192P 99US-0147303P 99US-014936P 99US-014936P 99US-014936P 99US-0149372P 99US-0149373P 99US-0151303P 99US-0151065P 99US-0153758P 99US-0153758P 99US-0153758P 99US-0153758P 99US-015365P 99US-0156458P 99US-0156458P 99US-015753P

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RESULT 9
ABA826222
ID ABA8
AC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comprising the vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a computation is differentially expressed in an animal subjected to pain and a computation is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying an agent compound that regulates the expression of the polynucleotide sequence the expressed in an animal subjected to pain, a method for identifying a compound which regulates compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity of an polynucleotide sequence the polynucleotide of a compound or small molecule that regulates the cativity in an animal of one or more of the polypoptides given in the specification, a method for identifying a compound useful in treating compained a pharmaceutical composition comprising the one or more compound that regulates the specification a method for identifying a compound useful in treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction conjury (CCI) and spazed nerve injury (SNI) in an animal (e.g. gene conjured that segmence presented is a rat DNA (shown in Table 2 of the specification) which encodes one of the polypoptides of the invention construction in the pattern in the pattern of the printed specification, but was contained in electronic form part of the printed specification, but was contained in electronic form directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                           antisense therapy; vaccine; bone osteomalacia; fibrous dysplasia;
   05-APR-2000;
05-APR-2000;
                                                                                         21-JUN-2000; 2000WO-US016951
                                                                                                                                                                                                                       WO200177327-A1
                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                        sequence tagged site; STS;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; high bone mass;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human HBM gene region b527d12-h_contig308G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA82622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA82622 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1144 BP; 310 A; 256 C; 291 G; 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page; 1017pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preparing
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GENBANK; Y00311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTAACACCTCGCAACTGGAGA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAACAACTCACAAATGGAGA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
   2000US-00543771.
2000US-00544398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33769
                                                                                                                                                                                                                                                                                                                                           osteoporosis; osteopathic; gene therapy; bone disorder; Paget's disease; scleros lasia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
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3;
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                                                                                                                                                                                                                                                                                                                                                                       sclerostosis;
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ABK22781
ID ABK22781
ID ABK22781
AC ABK22
XX ABC22
XX O9-AP
XX Human
XX Human
XX Human
XX Ostee
KW OST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                       diagnosing, treating or preventing e.g., identifying a molecule that binds to high corresponding wild type gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke; lipid-associated condition; arteriosclerosis; cardiovascular disease; ss osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up neurovascular condition; wound healing; gene therapy; PCR primer; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes the human Zmax1 gene and the high bone mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM genes have osteopathic activities. The genes can be used in gene therapy, antisense therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoporosis, the diagnosis and treatment of bone disorders including osteoporosis,
                                                                                                                                                                                                                                                                 Carulli JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human high bone mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New high bone mass (HBM) and Zmax1 genes and proteins useful modulating bone mass for the treatment of e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000; 2000US-00578900
                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001; 2001WO-US016946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200192891-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33769 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-657171/75
                                                                                                                                                      Identifying molecules involved in lipid regulation, useful for
                                                                                                                                                                                                             WPI; 2002-097784/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-) GENOME THERAPEUTICS CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         development
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18; Conserv
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                                                                                                                                                                                                                                                                 Little RD,
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                                                                                                                                                                                                                                                                                                                     CREIGHTON SCHOOL MEDICINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorder; antiarteriosclerotic; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA; 33769
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85.7%;
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                                                                                                                                                                                                                                                                 Recker RR,
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Pred. No. 3.
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                                                                                                                                                                                                                                                                 Johnson ML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; atherosclerosis; plaque build-up; gene therapy; PCR primer: nroh-clerotic: rard-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.4e+02;
                                                                                                     arteriosclerosis,
h bone mass gene o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ດ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 33769;
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                                                                                                                                comprises
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Example 2; Page 259-283; 409pp; English

gene

or

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RESULT 11
ACC45363
ID ACC45
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ACC ACC45
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ACC ACC45
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Humar
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Humar
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Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                  New transgenic animals (e.g. mice), useful as models for studying bone density modulation, developing drugs for treating or preventing bone diseases (e.g. osteoporosis), or diagnosing diseases characterized by reduced bone density.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-2001; 2001US-0290071P.
17-MAY-2001; 2001US-0291311P.
01-FEB-2002; 2002US-0351058P.
04-MAR-2002; 2002US-0361293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation; gene therapy; bone density modulation; bone strength; trabecular number; bone size; bone tissue connectivity; bone disease; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-129278/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAY-2002; 2002WO-US014876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-NOV-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human HBM gene fragment #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUN-2003
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WYETH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bex FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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85.7%;
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Pred. No. 3.4e+02;
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The invention relates bone mass (HBM) gene, Example 2; Page 323-334;

gene, expressing

to novel transgenic animals expressing expressing the corresponding wild type

the HBM high gene,

The present invention relates to High Bone Mass (HBM), LRP6 mutants, which results in a HBM-like phenotype when cell. The HBM-like phenotype results in bone mass modulat

modulation

ressed in a and/or lipid

LRP5 (Zmax1)

Example 3;

SEQ ID NO 8;

629pp; English.

603pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc comprising an alteration of the gene encoding LRP5 or LRP6, or expressing an LRP5 that is modulated by an altered gene control sequence introduced by homologous or non-homologous recombination. The transgenic animals are for the study of bone density modulation or bone mass modulation. The control may have a use in gene therapy. The transgenic animals and cultic acids are for the study of bone density modulation. The control may have a use in gene therapy. The transgenic animals and cultic acids are for the study of bone density modulation, where the complex in more than one parameter selected from bone density. Done strength, trabscular number, bone size, or bone tissue connectivity. The cultical compositions, which may be employed for treating or preventing bone compositions, which may be employed for treating or preventing bone cules involved in bone development, and for developing pharmaceutical compositions, which may be employed for treating or preventing bone cuseful in methods for diagnosing diseases involved in bone development, or characterised by reduced bone density or mass. The present sequence is or characterised by reduced bone density or mass. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 18
                                                                                                      New nucleic acid comprising a mutation in LRP5 or LRP6, useful for diagnosing a HBM-like phenotype in a subject and for preparing a composition for modulating bone mass and/or lipid levels in a subject
                                                                                                                                                                                                                                                                         11-MAY-2001; 2001US-0290071P.
17-MAY-2001; 2001US-0291311P.
01-FEB-2002; 2002US-0353058P.
04-MAR-2002; 2002US-0361293P.
                                                                                                                                                                     WPI; 2003-129214/12.
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                                                                                                                                                                                                                                                                                                                                                                                                               WO200292000-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
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                                                                                                                                                                                                                                              (GENO-)
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                                                                                        e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoporosis;
                                                                                                                                                                                                 Graham JR,
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Pred. No. 3.
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                                                                                                                                                                                                  Morales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human;
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                                                                                                                                                                                                 A,
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                                                                                                                                                                                                  Yaworsky PJ,
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level modulation.

The invention is useful for diagnosing a HBM-like bject and for preparing a composition for modulating

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ADESULT 13
ADES2432
ID ADES2
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Matches
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                                             The present invention relates to regulating LRP5, LRP6 or HBM activity is a subject comprising administering a composition which modulates a Dkk activity. The method is useful for modulating lipid levels and/or bone mass, and is useful in treating or diagnosing abnormal lipid levels and bone mass disorders, such as osteoporosis, bond fracture, age-related loss of bone, a chondrodystrophy, drug-induced bone disorder, high bone turnover, hypercalcaemia, hypercostosis, osteogenesis, imperfecta, osteomalacia, osteomyelitis, Paget's disease, osteoarthritis, and rickets. Modulators of Dkk activity are useful for as reagents in studying bone mass and lipid level modulation, in modulating Wnt signaling, or treating Dkk-mediated disorders. The present sequence represents a human DNA sequence related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regulating LRP5, LRP6 or HBM activity in a subject, useful for modulating lipid levels and/or bone mass, and for in treating bone mass disorders, e.g. osteoporosis, comprises administering a composition which modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Allen K,
Yaworsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAY-2001; 2001US-0291311P.
01-FEB-2002; 2002US-0353058P.
04-MAR-2002; 2002US-0361293P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 8; 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-129219/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyperostosis; osteogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRP5; LRP6; HBM; Dkk activity; Osteopathic; Antiinflammatory;
Antiarthritic; bone mass disorders; osteoporosis; hypercalcae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human DNA sequence related to
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85.7%;
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Pred. No. 3.4e+02;
0; Mismatches 3;
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Query Match

Sequence 33769

BP; 8178 A; 10222 C; 8617

G; 6749 T; 0 U; 3 Other;

Query Match Best Local S Matches 16

l Similarity 16; Conserv

Conservative

0;

Mismatches

0

Gaps

0

76.2%;

Score 16; Pred. No. C; 144

DB 6;

.1e+02;

Sequence

1118

BP; 389 A; 464

G;

121 T;

0 U; 0 Other; Length 1118; Indels

77.18;

Score 16.2;

BB

9

Length 33769;

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RESULT 14
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ID ABQ45
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                                              This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-CpG-3', present in a comethylation of a particular cytosine in a motif 5'-CpG-3', present in a comethylation of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, of oligomuclectides and/or peptide-nucleic acid (PNA) oligomers and the control of the amplicon. From the ratio of labels hybridised to the two classes of the amplicon. From the ratio of labels hybridised to the two classes of coligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central convous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (CNP's), and (ii) for differentiation of cell or tissue types and for convestigating cell differentiation. The method allows the methylation convestigating cell differentiation. The method allows the method the degree of cytosine methylation described in the control of the control of the degree of cytosine methylation described in the control of the cont
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05-SEP-2000;
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                                        disclosure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; 56pp + Sequence Listing; 56pp;
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2000DE-01044543
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                                          invention
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396

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                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpC-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC DNA that contains the target C is amplified to form a labeled amplicon. CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, CC degree of hybridisation to both classes is determined from the label on CC degree of hybridisation to both classes is determined from the label on CC cligomers, the degree of methylation is calculated. The method is used: CC if of a wide range of diseases, eg. cancer, disorders of the central CC enrous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms CC (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation CC tabgofall represent genomic DNA sequences used to illustrate the method CC disclosure of the invention
                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conserv
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05-SEP-2000; 2000DE-01044543.
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                                                                   CTAACACCTCGCAACT 708
                                                                                                                                                                                        76.2%; Score 16; DB 6; Le ilarity 100.0%; Pred. No. 3.1e+02; Conservative 0; Mismatches 0;
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Search completed: October 1, 2004, 03:41:21 Job time: 42.2571 secs

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Result
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Perfect score:
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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; TYPE: DNA
; ORGANISM: Fusarium solani
US-09-423-233-51
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US-09-423-233-51
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APPLICANT: The Government of the United States of America as TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus STITLE OF INVENTION: Other Filamentous Fungi FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51, Application Patent No. 6372430
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ALIGNMENTS

US/09423233

Species

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Sequence 6, Application US/09423233

Patent No. 6372430

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America as TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Spec TITLE OF INVENTION: Other Filamentous Fungi

FILE REFERENCE: 03063-0341WP

CURRENT APPLICATION NUMBER: US/09/423,233

CURRENT FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 61

SOUTWARE: Patentin Ver. 2.0

LENGTH: 319

TYPE: DNA

ORGANISM: Fusarium solani

US-09-423-233-6
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 21; Conservative 0
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Best Local
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Local Similarity 100.0%; Pred. No. 0.0
nes 21; Conservative 0; Mismatches
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  Score 21; DB 4; Length 319; Pred. No. 0.062; , Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (919) 541-8587
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/08905314A Patent No. 5827695
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                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                           FEATURE:

NAME/KEY: misc feature
LOCATION: 31..181
OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Fusarium avenaceum
INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
                                                                                                                                                                                   FEATURE:

NAME/KEY: misc_feature
LOCATION: 182.338
OTHER INFORMATION: /note
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (919) 541-8587
                                                                                                                                                                     EATURE:
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               NAME/KEY: misc_feature LOCATION: 505..561
OTHER INFORMATION: /note OTHER INFORMATION: rRNA
                                                                                                       NAME/KEY: misc feature LOCATION: 339.504
OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature LOCATION: 1..30
OTHER INFORMATION: /note OTHER INFORMATION: rRNA
                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: No. 5827695artis Corporation Patent Department STREET: 3054 Cornwallis Road CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222
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. Timothy
. 38,241
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             /note= "5'
rRNA gene"
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                                                                                                                                                                                                                                                                                                                                       rRNA gene"
                                                                                                             /note=
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                                                                                                                                                                                     "5.8S rRNA gene"
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                                 end of large subunit
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Query Match

90.5%;

Score 19;

DB 1;

Length 561;

; Sequence 120, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS

RESULT 5 US-08-311-731A-120/c

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US-08-956-171E-206/c
                                                                   Matches
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GENERAL INFORMATION:
                                                                                  Query Match
Best Local (
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                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 206: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
1809
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 206:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                16;
                               2 TAACACCTCGCAACTGG 18
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                                                                                  Similarity
TAATACCTCGCAACTGG
                                                                                                                                                                                         LENGTH: 29555 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                 TELEFAX: (301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 9410 Key West Avenue
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                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Michael R. Fannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craig A. Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; **.
                                                                                                                                                                              linear
                                                                                  73.3%;
                                                                                                                                                                                                                                                                                 309-8439
                                                                Score 15.4; DB 4; Length 29555; Pred. No. 1e+02; 0; Mismatches 1; Indels 0;
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; Mismatches
                                                                                                                                                                                                                                                                                                                                      PB248P1
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APPLICANT: MAO,

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US-08-311-731A-24/c
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US-08-311-731A-120
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/08311731A
Patent No. 6583266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION UNMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-2441
TELEPAX: 617/720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617/720-2441
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS:
               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               NEFAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 36181 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UZIP: 02210
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                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28405 AACACCGCGCAACTGGA 28389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 73.3%; Score 15.4; DB 4; Length 36181; Similarity 94.1%; Pred. No. 1.1e+02;
                                                                                                                                                                 BOSTON
                                                                                                                                         MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASSACHUSETTS
                                                                                                                                                                                  600 ATLANTIC AVENUE
                                                                                                                        USA
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PatentIn Release #1.0,
                                                                                                                                                                                                         WOLF,
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                                                                                                                                                                                                     GREENFIELD & SACKS, P.C
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Version #1.25
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TELEPAX: 617/720-2441
TELEPAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 38675 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-311-731A-135/c
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APPLICANT: SMITH,
APPLICANT: MAO, JF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
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NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                      ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOPTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                             CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DN
                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: I
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                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/311,731A FILING DATE:
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nes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 600 A
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TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 38494 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23279 CACCTCGCAACTGGCGA 23263
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                                                                                                                                                               31,616
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Pred. No. 1.1e+02;
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US-09-252-991A-6522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-398-858-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-398-858-13
                                                                                      GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1099-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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Matches
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Sequence 13, App
SEQ ID NO 6522
LENGTH: 927
                                                                                                                                                                                                                                                             Sequence 6522, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gregory, Carolyn A.
APPLICANT: McElver, John A.
APPLICANT: Hoesteter, George J.
TITLE OF INVENTION: Cyclin D Polynucloetides, Polypeptides
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 0926
CURRENT APPLICATION NUMBER: US/09/398,858
CURRENT FILING DATE: 1999-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lowe, Keith S. APPLICANT: Tao, Yumin APPLICANT: Gordon-Kamm,
                                                     PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-09-23
                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (1)...(1173)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1173
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                         CTAACAACCCTCAACTGGAG 569
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85.0%;
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Pred. No. 8
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Pred. No. 1.1e+02;
0; Mismatches 1
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US-08-311-731A-122
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                                                                                                                          Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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STREET
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NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: CO
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GRE
                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
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nes 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: doub
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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30961 AACACCTCGCGACTGGGG 30978
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                                                             AACACCTCGCAACTGGAG
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                                                                                                                              Conservative
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                                                                                                                                                             70.5%;
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                                                                                                                                                             Score 14.8; DB 4;
Pred. No. 2.3e+02;
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Pred. No. 1
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                                                                                                                                                                                           Length 41171;
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RESULT 11 US-09-198-452A-1

Sequence 1, Application US/09198452A Patent No. 6559294 GENERAL INFORMATION:

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SEQ ID NO 1
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TYPE: DNA
ORGANISM: Chlamydia preature:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preventation of inventation treatment of infection FILE REFERENCE: 9710-003-999

CURRENT FILE TAPPLICATION NUMBER: US/09/198,452A

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
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                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (225001)..(240000)
OTHER INFORMATION: n=a or c or
                                    NAME/KEY: misc_feature
LOCATION: (270001)..(285000)
OTHER INFORMATION: n=a or c or
                                                                               OTHER INFORMATION: n=a or c or
                                                                                                                         OTHER INFORMATION: n=a or c or
                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (195001)..(210000)
OTHER INFORMATION: n=a or c or
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LOCATION: (1)...(15000)
OTHER INFORMATION: n=a or
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OTHER INFORMATION: n=a or c or
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OTHER INFORMATION: n=a or c or
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OTHER INFORMATION: n=a or c
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.OCATION: (255001)..(270000)
                                                                                                                                         JAME/KEY: misc_feature
JOCATION: (240001)..(2
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THER INFORMATION: n=a or c or
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OCATION: (165001)..(180000)
WHER INFORMATION: n=a or c or
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OCATION: (150001)..(165000)
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OTHER INFORMATION: n=a or c or
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THER INFORMATION: n=a or c or
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JOCATION: (300
                AME/KEY: misc_fea
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ICCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
LOCATION: (645001)..(660000)
OTHER INFORMATION: n=a or c or g LOCATION: (405001)..(420000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (420001)..(435000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (435001)..(450000)
OTHER INFORMATION: n=a or c or NAME/KEY: misc_feature LOCATION: (570001)..(585000) OTHER INFORMATION: n=a or c LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc_feature NAME/KEY: misc feature LOCATION: (585001)..(600000) OTHER INFORMATION: n=a or c NAME/KEY: misc_feature LOCATION: (525001)...(540000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc_feature
LOCATION: (540001)...(555000) NAME/KEY: misc feature LOCATION: (300001)..(315000) OTHER INFORMATION: n=a or c LOCATION: (555001)..(570000)
OTHER INFORMATION: n=a or c NAME/KEY: misc_feature LOCATION: (480001)..(495000) OTHER INFORMATION: n=a or c OTHER NAME/KBY: misc_feature LOCATION: (465001)..(480000) OTHER_INFORMATION: n=a or c NAME/KEY: misc feature LOCATION: (450001)...(465000) OTHER INFORMATION: n=a or c NAME/KEY: misc_feature LOCATION: (345001)..(360000) OTHER INFORMATION: n=a or c LOCATION: (315001)..(330000)
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Best Local S
Matches 16
                                                                                                                        Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
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LOCATION: (840001) .. (855000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
LOCATION: (855001) .. (870000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
LOCATION: (870001) .. (885000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (765001)...(780000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
LOCATION: (780001)...(795000)
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           APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (900001)...(915000)
OTHER INFORMATION: n=a or c
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LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c
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LOCATION: (825001)...(840000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (810001)..(825000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (720001)...(735000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (675001)..(690000)
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LOCATION: (795001). (810000)
OTHER INFORMATION: n=a or c
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NAME/KEY: misc_feature
LOCATION: (75001)...(765000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (735001)..(750000)
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REFERENCE: 24366-20007.00
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CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 SEQ ID NO 5642 LENGTH: 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                     Sequence 5642, Application Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
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Patent No. 6294328
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Best Local
                                                                                                                           APPLICANT: GATY Breton et. al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DUA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
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OTHER INFORMATION: "n" bases at various
OTHER INFORMATION: represent a, t, c or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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88.9%;
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Pred. No. 1.
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Pred. No. 1.
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Mismatches 2;
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ORGANISM: Klebsiella pneumoniae

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
CLASSIFICATION INDATA:
APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
CLASSIFICATION NUMBER: 40/079,677
FILING DATE: March 27, 1998
CLASSIFICATION NUMBER: 42,918
CLASSIFICATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: 42,918
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: 9A-0008 US
TELECOMMUNICATION INFORMATION:
TELEPAN: (650) 845-4166
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: Sinear
                                                                                                                                                                     ; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGTUTO8
; CLONE: 2642108
US-09-276-531-122
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US-09-276-531-122
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                                                                                Query Match 69.5%; Score 14.6; DB 3; Best Local Similarity 81.0%; Pred. No. 1.5e+02; Matches 17; Conservative 0; Mismatches 4;
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Patent No. 6183968
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APPLICANT: Yue, Henry
APPLICANT: Reddy, Goopa
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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442 CTAAAACTTTGTAACTGGAGA 462
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Hillman, Jennifer L.
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Search completed: October 1, 2004, 08:06:04 Job time: 26.9205 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0 seq length: 2000000000
Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

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14: /cgn2_6/ptodata/1/pubpna/US09NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US09NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US09NEW_PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10R_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10R_PUB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10R_PUB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10R_PUB.seq:*
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21
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Copyright (c) 1993 - 2004 Compugen Ltd.
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1244.847 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	n	Result
10 12 13	8 1 2 3 3 4 4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0 t
16.2 16.2 16.2 16.2	16.21 16.21 16.22	Score
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1037 1037 1037 1037 1037 1037	3 21 403 499 499 499 894	Length DB
13 13 16 16	15 13 13 13 14 16	BB
US-10-027-632-259445 US-10-027-632-259446 US-10-027-632-259447 US-10-027-632-259445 US-10-027-632-259445 US-10-027-632-259446 US-10-027-632-259446	US-10-046-955-51 US-10-046-955-6 US-10-424-599-123319 US-10-027-632-136133 US-10-027-632-136134 US-10-027-632-136134 US-10-027-632-136134 US-10-027-632-136134	ID
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Sequence 32, Appl	# 2 C				206,	Sequence 206, App	Sequence 16977, A	Sequence 7697, Ap	Sequence 8805, Ap	Sequence 8175, Ap	Sequence 4687, Ap	Sequence 11, Appl	Sequence 8995, Ap	Sequence 25297, A	Sequence 1, Appli	Sequence 655, App	Sequence 3724, Ap	Sequence 3726, Ap	Sequence 6673, Ap	95510	Sequence 656, App	Sequence 33226, A		1408	10	8	Sequence 8, Appli	

ALIGNMENTS

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APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 1908-05-01
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEO ID NOS: 61
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                 ; SEQ ID NO 51
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Fubarium solani
US-10-046-955-51
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US-10-046-955-51
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                                                                     Best Local
Matches 2
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APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Diseapplicant: Control and Prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51, Application US/10046955
Publication No. US20030129600A1
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
1 CTAACACCTCGCAACTGGAGA 21
                                                                     ch 100.0%; Score 21; DB | Similarity 100.0%; Pred. No. 0.6; 21; Conservative 0; Mismatches
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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
US-10-046-955-6
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                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_82365C.1
US-10-424-599-123319
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LENGTH: 403
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                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10046955
Publication No. US20030129600A1
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/045,400 PRIOR FILING DATE: 1997-05-02
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CURRENT FILING DATE: 2002-06-04
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APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species
TITLE OF INVENTION: Other Filamentous Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: The Government of the United States of APPLICANT: Secretary of the Department of Health APPLICANT: Control and Prevention APPLICANT: Morrison, Christine J.
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
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                                                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                                                                                                                                                                                              TYPE: DNA
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Local Similarity 100.0%; Score 21;
Local Similarity 100.0%; Pred. No.
les 21; Conservative 0; Mismatch
                                                                                                          Local
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                             1 CTAACACCTCGCAACTGGAGA 21
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CTAACAGCACACAACTGGAGA 127
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85.7%;
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US-10-027-632-136134
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US-10-027-632-136133
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US-10-027-632-136133
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Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 136133
LENGTH: 499
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 136134
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Best Local Similarity
                                                                      PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                 NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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85.7%;
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Pred. No. 2e+02;
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US-10-027-632-136134
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US-10-027-632-136133
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US-10-027-632-136133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-08-09
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Best Local Similarity
Matches 18; Conser
                                                                                                                                                                                                                                                                                                                                                      Sequence 136134, Application US/10027632 Publication No. US20030204075A9
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                                                                    APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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TYPE: DNA
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                          APPLICATION NUMBER: US 60/193,483 FILING DATE: 2000-03-29
APPLICATION NUMBER: US 60/185,218
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85.7%;
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85.7%;
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Pred. No. 2e
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Pred. No. 26
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 41403

LENGTH: 894

TYPE: DNa
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Sequence 259445, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
APPLICANTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 136134
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-08-09 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: PAT_MRT4530_44751C.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                      763 CTGACCCCTCGAAACTGGAGA 743
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85.7%;
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85.7%;
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Pred. No. 2
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Pred. No. 26
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2e+02;
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CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR PRILING DATE: 1999-10-28

PRIOR PRILING DATE: 1999-09-28

PRIOR PRILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09
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US-10-027-632-259445
                                                                                                               Query Match
Best Local Similarity
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SEQ ID NO 259446
                                                                                            Matches
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SEQ ID NO 259445
LENGTH: 1037
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Best Local Similarity 85.7%;
Matches 18; Conservative
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
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FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
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496 CTTACCCCTTGCAACTGGAGA 516
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                              1 CTAACACCTCGCAACTGGAGA 21
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                                                                                         Conservative
                                                                                                                                                                                                                                                                                           for Windows Version 4.0
                                                                                                            77.1%;
85.7%;
                                                                                     Score 16.2; DB Pred. No. 2e+02; 0; Mismatches
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Pred. No. 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2e+02;
                                                                                                                                  DB 13;
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                                                                                                                               Length 1037;
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RESULT 11 US-10-027-632-259447

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US-10-027-632-259445
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US-10-027-632-259445
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                                                                     SOFTWARE: FastSEQ for Windows
SEQ ID NO 259445
LENGTH: 1037
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 259447
LENGTH: 1037
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Best Local Similarity
Matches 18; Conserv
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Publication No. US20020198371A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                 NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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PRIOR APPLICATION NUMBER: US 60/146,002
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                  ORGANISM: Human
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23
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Query Match

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                                     CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 259446
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
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APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23
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Pred. No. 2e+02;
0; Mismatches 3;
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Pred. No. 2e+02;
0; Mismatches 3;
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; ORGANISM: Human
US-10-027-632-259447
                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96920C.1
US-10-437-963-99074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-437-963-99074
                                                                                                                                                                                                   TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 99074 LENGTH: 2985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 259447
LENGTH: 1037
                                                              Matches
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Best Local
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                                                                                                                                                                   ORGANISM: Oryza sativa
                                                                                                                                                                                          TYPE: DNA
                                                                           Local Similarity
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1071 CTAACTCCTCGCAGTTGGAGA 1091
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                             CTAACACCTCGCAACTGGAGA 21
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Wu, Wei
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                                                            Conservative
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US20040123343A1
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Pred. No. 2
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Minimum
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Maximum Match 100%
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                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2133.013 Million cell updates/sec
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 CE746752
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0330 vw91d02	AA840330	9		77.1	16.2	4.3
83642	AQ836420	28	430	77.1	. 0	42
0150 ZMMBBC	CC930150	29	384	77.1	σ,	41
13861 RPCI11	AQ013861	28	349	77.1	ο,	40
50963 CITBI-E	AQ260963	28	326	77.1	ა	39
5 BB5723	BB572305	10	293	77.1	9	38
089128 BB08912	B08912	10	293	7	16.2	
43034 AV043034	43C	ø	266	7	٥,	36
Z468148 1M0281F	AZ468148	28	252	7	σ.	<u>3</u> 5
H061403 RPCI-24-	BH061403	28	819	8		34
61459 RPCI-24-	BH061459	28	787		•	33
7 CH240 42	CC546447	29	771	•	16.4	32
3 RPCI-24-	BH064238	28	713		ა.	31
619904 HVSMEc	BF619904	10	587	80		30
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582687 RC0-ST0	AW582687	10	469	8	٥.	28
9 BJ12596	ВJ125969	12	394	78.1	16.4	27
BJ1543	ВЛ154339	12	380	78.1	16.4	26
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2356	CNS0777Y	29	972		σ.	20
G114704 PUFMO8	1470	29	951		σ	19
2659389 OGAME36	BZ659389	28	907		σ,	
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ALIGNMENTS

CE746752

CE746752

INITION Ligr-gss-dog-17000369563878 Dog Library Canis familiaris genomic, genomic survey sequence.

SSSION CE746752.1 GI:37087099

WORDS CEDIA Familiaris (dog)

CE746752.1 GI:37087099

WORDS Canis familiaris (dog)

CEANISM Enalitaris (dog)

CANIS Familiaris (dog)

CANIS FAMMANIA; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 762)

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 762)

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 762)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rugch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.

The dog genomic survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)

DLINE The dog genomic Survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)

DLINE The dog genomic Research Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0200

Fax: 301-838-0200

Email: ekirknessetigr.org

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RESULT 3
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606 bp mRNA linear EST 06-NOV-200.
81-E011664-027-006-A22-T7R MPIZ-ADIS-027 Arabidopsis thaliana cDNA
clone MPIZp772A228Q 5-PRIME, mRNA sequence.
CB256360
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Low-pass Sequencing for Microbial Comparative Genomics Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natrialba asiatica
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ygoo@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institute for Systems Biology
1441 North Street, Seatt
Tel: 206 732 1412
Fax: 206 732 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2
Contact: Goo Y
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19; Conservative
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                                                                                                                                                                                                                                                            /clone lib="Na pUC18 Library"
/note="Vector: pUC18; Site 1: SmaI; A shotgun library
constructed from Natrialba asiatica genomic DNA using
pUC18/SmaI/BAP plasmid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                       /organism="Natrialba asiatica"
/mol_type="genomic DNA"
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/strain="ATCC 700177"
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0; Mismatches 2;
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Pred. No. 9.
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9.9e+02;
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T., Mitchell-Olds, T. and Weisshaar, B.
Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thal Genome Res. 13 (6), 1250-1257 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 606 Std Error: 0.00
Plate: 6 row: A column: 22
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
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                                                                                                                                                                  Conservative
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T7-SalI-CCACCGTCGC-Sprime-cDNA-polyA-CC-NotI-Sp6; Note:
Sequencing granted in the context of the GABI Arabidopsis verbund I: Genetic Diversity, 'Sstablishment of high-efficiency SNP-Dased mapping tools and development of methods for genome-wide mutation detection, PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further
                                                                                                                                                                                                                                                                        information."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="whole plant"
/dev_stage="adult plant, mixed stresses"
/lab_host="E. coli TOP10"
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/cultivar="Eifel-2 (Ei-2)"
/db_xref="GABI:593758"
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r: T7R; CTAATACGACTCACTATAGGGA.
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tive 0;
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100.0%; Pred. No.
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DEFINITION

AG225492 313 bp Lotus corniculatus var. japonicus

DNA linear GSS 19-JUL-2003 DNA, clone:LjB12h04_f, genomic

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RESULT 5
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                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 362)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 bp mRNA linear
RC3-BT0502-251199-011-b12 BT0502 Homo sapiens cDNA,
BE070797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute The First Laboratory for Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (B-mail:ssato@kazusa.orjp, URL:http://www.kazusa.or.jp/en/plant/, Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sato, S., Nakamura, Y. and Tabata, S. Lotus japonicus BAC End sequences Published Only in Database (2002) 2 (bases 1 to 313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Vagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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AG225492
AG225492.1 GI:26536116
GSS.
                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Res.
Rua Prof. Antonio Prudente 109,
                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                     sequence tags
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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/mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/variety="japonicus"
/db xref="taxon:34305"
/clone="tijbliblo4 f"
/clone="tijb="genomic BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="VECTOR:pBeloBAC11~synonym: Lotus japonicus"
                                                                                                                                                                     Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 1.6e+03;
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High quality sequence start: 28 High quality sequence stop: 362. Location/Qualifiers
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-BT0502-251
199-011-b12&t3=1999-11-25&t4=1)
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                                                                 90.0%;
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                                                                 Score 16.8; DB 10
Pred. No. 1.7e+03;
       Mismatches
                                                                                                                                   10;
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<u>.</u>
       Gaps
       0
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Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com)
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2142 row: I column: 8
Seq primer: M13 Reverse High Throughput Sequencing Couniversity of Washington 401 Queen Anne Avenue North, Tel: (206) 616-3618
Fax: (206) 616-3887 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 1 (bases 1 to 458)
Mahairas,G.G., Wallace,J.C., Smith,K.,
Keller,A., Shaker,R., Furlong,J., Youn AQ681735 458 bp DNA HS_2142_A2_E04_MR CIT Approved Human Ge sapiens genomic clone Plate=2142 Col=8 10449764 Contact: Mahairas GG, Wallace JC, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AQ681735 AQ681735.1 99380589 Homo sapiens Class: BAC ends Homo sapiens (human) quality sequence stop: 458.
Location/Qualifiers /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" . 458 GI:5257718 Center Seattle, Hood Young, Genomic Sperm Library D Homo =8 Row=I, genomic survey WA 98109, Swartzell,S., g,J., Zhao,S., linear Holzman, T. Adams, M.D. GSS 28-JUN-1999 and

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SP 1019_A1 A04 SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus purpuratus cenomic clone Plate=1019 Col=7 Row=A, genomic survey sequence AZ191211

AZ191211.1 GI:8374390
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Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cameron, RA, Davidson, EH.
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: acameron@caltech.edu
Plate: 1019 row: A column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         additional resources Proc. Natl. Acad. Sci. U.S.A.
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Location/Qualifiers
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(626) 793-3047
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                                                                                                                                                                                                        /organism="Strongylocentrotus purpuratus"
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/db_xref="reaxon:7668"
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/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-DH10B"
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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BM440563
BM440563.1 GI:18471338
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717,
Tel: 302-831-1335
                                                                1 (bases 1 to 610)
Cogburn, L. A. and Nys, Y.
ESTs from Normalized Chicken Reproductive Tract cDNP
University of Delaware and INRA, Tours-Poultry Unit
Unpublished (2002)
                                                                                                                                                                                                      Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>بـ</del>
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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RESULT

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Project

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551 CCÁACACCTTGCÁACTGGÁG 570
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1 (bases 1 to 586)

Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M.

Taylor,R., Ashurst,J.L., Eroning,M.D.R., Zorn,A.M.

Sanger Xenopus tropicalis EST project 2002

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing primer: SP6
This sequence is from a Xenopus
constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas124m04.plcSP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST. Silurana tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL955976 XGC-gastrula Silurana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hinxton, Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Silurana tropicalis
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                                                                                                         Similarity
                               CTAACACCTCGCAACTGGAG
                                                                                     Conservative
                                                                                                                                                                                                          /clone lib="XGC-gastrula"

/note="Vector: pCS107; Site 1: ECORI; Site 2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. ECORI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3'
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                        /dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
                                                                                                                                                                                                                                                                                                                                                                     lone="TGas124m04"
                                                                                                         80.0%;
90.0%;
                                                                                   0
                                                                                                       Score 16.8; DB
Pred. No. 2e+03;
                                          20
                                                                                     Mismatches
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TGas124m04 5',
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                                                                                   Gaps
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REFERENCE
AUTHORS
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KEYWORDS
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CG294089
LOCUS
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Best Local Similarity
Matches 18; Conserv
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 639)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw, C.A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG294089
OG1BI82TH ZM_0.7_1.5_KB
                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
Other_GSSs: OG1B182TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG294089.1 GI:34208303 GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 302-831-2822
Email: cogburn@ud
                                                                                                                                                                                                                                Class: sheared ends.
                                                                                                                                                                                                                                                Seq primer: TR
                                                                                                                                                                                                                                                                              Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                              Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays
                                                                                                                                                                                                                                                             Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAGACCTCGCAAATGGAGA 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAACACCTCGCAACTGGAGA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cogburn@udel.edu, www.chickest.udel.edu.
                                                              /clone="ZMMBMa0723N19"
/clone_lib="ZM_0.7_1.5_KB"
/notee="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic_DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Vector: pCMVSPORT6; Library made from three total
RNA pools from each tissue (testis 25%, ovary 25%, and
oviduct 50% of final RNA pool); Single pass sequencing
from 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Various stages;embryonic, post-hatch, immature
and sexually-mature"
/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Commercial broiler
/db_xref="taxon:9031"
                                                                                                                                               /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                'db_xref="taxon:4577"
                                                                                                                                                                              organism="Zea mays"
                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Normalized Chicken Reproductive
ibrary (pgrln)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="Testis, ovary and oviduct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="pgrln.pk003.h4"
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   90.0%;
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Pred. No. 2e+03;
   Score 16.8; DB 29; Pred. No. 2e+03;
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                  RESULT 12
BU235239
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MEDLINE
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Matches
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Matches
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286 TAAGACCTCGCAAATGGAGA 305
                                                                                            18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (chicken)
Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22335534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12445392
                                                                                                                   Similarity
                              TAACACCTCGCAACTGGAGA 21
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                                                                                       80.0%;
nilarity 90.0%;
Conservative
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                                                                                                                                                                                                        /clone lib="CSEQCHN59"
//clone lib="CSEQCHN59"
//note="Organ: limbs; Vector: pBluescript II KS(+); Site 1:
//note="Organ: limbs; Vector: pBluescript II KS(+); Site 1:
// note="Organ: limbs; Vector: pBluescript II KS(+); Site 1:
// note="Organ: limbs; Vector: pBluescript was
constructed from 1 million independent clones: cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
// pollowing this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dev_stage="36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="ChEST973o12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:9031"
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                                                                                                                   Score 16.8; DB 13; Pred. No. 2e+03;
                                                                                            Mismatches
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                                                                                                                                             646;
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EST 26-NOV-2002

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RESULT 13
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                            sequence.
BU482142
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603841434F1 CSEQRBN22 Gallus
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1 (bases 1 to 668)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                  BU482142.1 GI:25975719
                                                                                                                                                                                                                                                                            BU482142
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University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO Box 88, Manchester, M60 1QD, Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simon Hubbard
Department of Biomolecular Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12445392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strāin="White Leghorn, Hisex"
/db xref="taxon:9031"
/clone="ChEST759n10"
/dev stage="22"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_lib="CSEQCHN24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.8;
Pred. No. 2.
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                                                                                                                                                                                                                                             gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 668;
                                                                                                                                                                                                                                                                            linear
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BU311672
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                                                                                TITLE
                                                                                                                                      AUTHORS
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                                                                          Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 784)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
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603541288F1
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Mismatches

21

bp mRNA linear EST 28 gallus cDNA clone ChEST510p21

28-NOV-2002 p21 5', mRNA

Score 16.8; DB 13 Pred. No. 2.1e+03;

DB 13;

Length 679;

0,

Gaps

0

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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., I Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 679)
/Clone lib="CSEQRBN22"
//Clone lib="CSEQRBN22"
//Clone lib="CSEQRBN22"
//note="Vector: pBluescript II KS(+); Site 1: EcoRI;
//note="Vector: pBluescript II KS(+); Site 1: EcoRI;
//note="Vector: pBluescript II KS(+); Site 1: EcoRI;
Site 2: Not1; This normalized library was constructed from
1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was blunted, ligated to
NotI adapters, digested with EcoRI, size-selected, and
cloned into the NotI and EcoRI compatible sites of a
custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldo et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
used."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="Layer and broiler"
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REFERENCE
AUTHORS
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DEFINITION
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BU330991
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    FEATURES
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Best Local Similarity
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                                                                                                                                                                                                                                               Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 811)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                     Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU330991 811 bp mRNA linear EST 28-NOV-2002 603870435F1 CSEQCHN65 Gallus gallus cDNA clone ChEST896e9 5', mRNA
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Location/Qualifiers
                                              Fax: 01612360409
                                                                                         PO Box 88, Manchester,
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                                                                                                                      (TSIMU)
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/clone="Organ: heart; Vector: pBluescript II KS(+); Site_1:
/note="Organ: heart; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994): 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996: 791, except that a significantly longer
reannealing hybridization was used."
Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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/strain="Compton Line 151"
/db_xref="taxon:9031"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="ChEST510p21"
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Query Match Best Local

Local Similarity

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Score 16.8; DB 13; Pred. No. 2.2e+03;

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Search completed: October 1, 2004, 08:01:59 Job time: 302.333 secs This Page Blank (USDIO)

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SUMMARIES

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Result No. Score Query Match 00 Length DВ AR206443 AR206401 BD083592 AF162903 AF502789 AF502716 AF502716 AF502717 AF502717 AF502714 AF5 ij NF493963 AF493965 AF493966 AF261740 AF2286663 AJ228666 AJ228666 AJ228666 AJ228666 AJ228667 AJ228667 AJ228677 AF502667 AF502716 AF111060 AF502714 AF261745 AF502641 AF502843 AF502789 AF117922 AF162903 AR206401 BD083592 AY243055 AF430128 AR206443 Description Nectria g Sequence Nucleic a Nectria Nectria

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AR206443 Sequence 49 from AR206443 AR206443.1 GI:2 Unknown. Unknown. Unclassified. 1 (bases 1 to 1) Morrison, C. J., R Nucleic acids fo filamentous fung Patent: US 63724	JOURNAL	BTILL	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AR206443	RESULT 1
18 bp DNA linear PAT 20-JUN-2002 patent US 6372430. 1505046 1505046 8) 8) 8) 62 c	filamentous fungi Patent: US 6372430-A 49 16-APR-2002;	Nucleic acids for detecting Aspergillus species and other	Morrison, C.J., Reiss, E., Aidorevich, L. and Choi, J. Soo.	1 (bases 1 to 18)	Unclassified.	Unknown.	Unknown.		AR206443.1 GI:21505046	AR206443	Sequence 49 from patent US 6372430.	DNA linear		

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I (bases 1 to 18)

R (bases 1 to 18)

Rorrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.

Nucleic acids for detecting Aspergillus species and other
filamentous fungi

L Patent: JP 2001525665-A 49 11-DEC-2001;

THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O
CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND
PREVENTION TECHNOLOGY TRANSFER OFFICE
OS FUSARium moniliforme
PN JP 2001525665-A/49

PD 11-DEC-2001

PT 01-MAY-1998 JP 1998548275
PR 02-MAY-1997 US 60/045400

PI CHGISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO
PI CHOI
CHOI
CC Strandedness: Single;
CC Topology: Linear;
FH Key Total Control of the Control
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AR206401
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Gibberella fujikuroi
Gibberella fujikuroi
Gibberella fujikuroi
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
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/mol_type="genomic DNA"
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Gibberella fujikuroi
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Patent: US 6372430-A 7 16-APR-2002;
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Morrison, C.J., Reiss, E., Aidorevich, L. and Choi, J.
Nucleic acids for detecting Aspergillus species an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .310
                                                                                             /organism="Gibberella fujikuroi"
/mol_type="genomic DNA"
/db_xref="taxon:5127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.18;
94.48;
                                                  91.1%;
94.4%;
191
                                        0,
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                                        Score 16.4; DB 6;
Pred. No. 3.3e+02;
0; Mismatches 1
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Pred. No. 3.3e+02;
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                                                            DB 6;
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                                                            Length 310;
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JOURNAL
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174
                                                                                                                            Direct Submission
Direct Submission
Submitted (28-JUN-1999) Biology, SangMyung University,
Submitted Ro-Gu, Secul 110-743, Korea
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP117922 310 bp DNA linear PLN 17-JUN-2000 Gibberella fujikuroi ATCC 38519 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                              Fusarium proliferatum
Fusarium proliferatum
Eusarium proliferatum
Eusarium proliferatum
Eusarium proliferatum
Eusarium proliferatum
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Eusarium proliferatum

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA gene, partial sequence.
AF162903
AF162903.1 GI:5690392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998) 2 (bases 1 to 310) Choi.J.S., Westerman, J.M. and Morrison, C.J. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 310)
Choi, J.S., Westerman, J.M. and Morrison, C.J.
Rapid differentiation of filamentous fungi using species-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-SEP-1998) DBMD, 30333, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreomycetidae; Hypocreales; Nectriaceae; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gibberella
                                                                                                                                                                                                                                                                                         Min, B.R.
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/organism="Fusarium proliferatum"
/mol type="genomic DNA"
/strain="6787"
/db_xref="taxon:42674"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:5127"
<1._.159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="5.8S ribosomal RNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.4; DB 8;
Pred. No. 3.3e+02;
0; Mismatches 1;
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Gibberella; Gibberella
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nes 17; Conserv
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sequence.
AF502789
AF502789.1
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                                        AF502789 393 bp DNA linear PLN 13-MAY-2002 Leaf litter ascomycete strain its265 isolate 1000143643 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial
                                                                                                                                                                                              μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota.

1 (bases 1 to 392)

Gilbert, G.S., Garbelotto, M., Chapela, I.,
Dreyfuss, M.M.

Biogeography of leaf litter fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF502843

392 bp DNA linear PLN 13-MAY-2002 leaf litter ascomycete strain its332 isolate 1000096451 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 392)
Gilbert, G.S., Garbe
Dreyfuss, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leaf litter ascomycete strain leaf litter ascomycete strain
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                                                                                                                                                                                                                             Conservative
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129. .293
                                                                                                                                                                                                                                                                                                      /note="contains internal transcribed spacer 1,
ribosomal RNA and internal transcribed spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                country="Puerto Rico"
                                                                                                                                                                                                                                                                                                                                                                 'specific_host="Prestoea
'db_xref="taxon:194115"
                                                                                                                                                                                                                                                                                                                                                                                               'isolate="1000096451"
                                                                                                                                                                                                                                                                                                                                                                                                                               ao_
                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="leaf litter ascomycete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="28S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                             strain="its332"
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 GI:20531596
                                                                                                                                                                                                                                        91.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                          _type="genomic DNA"
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94.4%;
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                                                                                                                                                                                                                                          Score 16.4; DB 8;
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.4; DB 8;
Pred. No. 3.3e+02;
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its332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moeller, C.
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                                                                                                                                                                                                                                                          Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                           strain its332"
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TITLE
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AUTHORS
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AF502667
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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JOURNAL
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JOURNAL
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Best Local
                                                                                                                                                                                                 AUTHORS
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AF502667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leaf litter ascomycete strain its265
leaf litter ascomycete strain its265
Eukaryota, Fungi, Ascomycota.
1 (bases 1 to 393)
Gilbert,G.S., Garbelotto,M., Chapela,I.,
                                                                                                                              Submitted (12-APR-2002) Environmental Studies, Uni California, Santa Cruz, 1156 High St., Santa Cruz,
                                                                                                                                                                              2 (bases 1 to 402)
Gilbert,G.S., Garbelotto,M.,
Dreyfuss,M.M.
                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota.

1 (bases 1 to 402)

Gilbert,G.S., Garbelotto,M., Chapela,I.,
Dreyfuss,M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                AP502667 402 bp DNA linear PLN 13-MAY-2002 Leaf litter ascomycete strain its086 isolate 1000589588 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 393)
Gilbert,G.S., Garbelotto,M., Chapela,I.,
Dreyfuss,M.M.
                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                Biogeography of leaf litter fungi
                                                                                                                                                                                                                                                                                                                                                                                                                               transcribed spacer complete sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biogeography of leaf litter fungi
Unpublished
                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                             leaf litter ascomycete strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTAGTGACGGTCTCGCT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
/isolate="1000589588"
/specific_host="Brosimum
/db_xref="taxon:193939"
                                                                /organism="leaf litter ascomycete
/mol_type="genomic DNA"
                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /specific_host="Prestoea
/db_xref="taxon:194061"
/country="Puerto Rico"
                                                   strain="its086"
                                                                                               . .402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="its265"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="leaf litter ascomycete strain its265"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolate="1000143643"
                                                                                                                                                                                                                                                                                                                                                                                  GI:20531474
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94.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 393;
                                                                                strain its086'
                                                                                                                                University
cuz, CA 9506
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RESULT 11
AF111060
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AUTHORS
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Best Local S
Matches 17
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JOURNAL
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                                                                        353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342
                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission

Submitted (12-APR-2002) Environmental Studies, University of Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF502716 418 bp DNA linear PLN 13-MAY-2002 Leaf litter ascomycete strain its182 isolate 1000011379 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 418)
Gilbert, G.S., Garbelotto, M., Chapela, I.,
Dreyfuss, M.M.
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Gilbert, G.S., Garbelotto, M., Chapela, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biogeography of leaf litter fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leaf litter ascomycete strain
leaf litter ascomycete strain
Bukaryota; Fungi; Ascomycota.
                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dreyfuss,M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                TCTAGTGACGGTCTCGCT 18
                                                                                                                               Conservative
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                                                                                                                                                                                                                 /product="5.8S ribosomal 293. .>418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="5.8$ ribosomal 276. .>402
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/product="internal transcribed 121. .275
                                                                                                                                                                                                                                                                                                                                            /organism="leaf litter ascomycete strain its182"
/mol_type="genomic_DNA"
/strain="its182"
                                                                                                                                                                                                     /product="internal transcribed
                                                                                                                                                                                                                                                                           country="Panama":1. .137
                                                                                                                                                                                                                                                                                                    /specific_host="Coussapoa
/db_xref="taxon:193988"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /country="Panama"
                                                                                                                                                                                                                                                                                                                                'isolate="1000011379"
                                                                                                                                                                                                                                                          product="internal transcribed
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                                                                                                                                        91.18;
94.48;
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94.4%;
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                                                                                                                            Score 16.4; DB 8;
Pred. No. 3.3e+02;
0; Mismatches 1
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Pred. No. 3.
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                                                                                                                                                        Length
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                                                                                                                               Indels
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                                                                                                                                                           418;
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DEFINITION

AF111060 419 bp DNA Fusarium sublunatum var. sublunatum stratranscribed spacer 1, partial sequence;

DNA linear PL strain BBA62431 int nce; 5.8S ribosomal

PLN 20-JAN-1999

complete

and internal transcribed spacer

2, partial

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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
                                                                                                         JOURNAL REFERENCE
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AF430128
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AUTHORS
TITLE
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VERSION
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                                               TITLE
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Best Local Similarity
                                                                                     AUTHORS
                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
Direct Submission
Submitted (09-OCT-2001) Forestry and Agricultural Biotechnology
Institute (FABI), University of Pretoria, Lunnonstreet, Pretoria,
                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari 1 (bases 1 to 421)

Britz,H., Coutinho,T.A., Wingfield,B.D., Marasas,W.F.O. and Wingfield,M.J.
                                                                                                                                                                                                                                                                                                                                                                                          AP430128 421 bp DNA linear PLN 06-NOV-Fusarium mangiferae strain MRC3477 185 ribosomal RNA gene, part sequence; internal transcribed spacer 1 and 5.85 ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 419)
Bulat, S.A. and Alekhina, I.A.
Direct Submission
Submitted (03-DEC-1998) Department of Molecular and Radiation
Biophysics, Petersburg Nuclear Physics Institute RAS, Gatchina,
Leningrad Region 188350, Russia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bulat, S.A., Yli-Mattila, T. and Alekhina, I.A. Molecular taxonomy of Fusarium strains by means of ribotyping, sequencing and UP-PCR analysis. A case study of Sporotrichiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusarium sublunatum var. sublunatum Eusarium; Sordariomycetes; Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreomycetidae; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

1 (bases 1 to 419)
                                                                                 2 (bases 1 to 421)
Britz,H., Coutinho,T.A.,
                                                                                                                                           Vegetative compatibility and distribution of two Fusarium species associated with mango malformation in South Africa
                                                                                                                                                                                                                                                                             Fusarium mangiferae
Fusarium mangiferae
                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                        AF430128.1 GI:24637153
                                                                                                                                                                                                                                                                                                                                                                                sequence.
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                                                                     Wingfield, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jnpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTAGTGGCGGTCTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="internal transcribed
/note="ITS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="5.8S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:86548"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variety="sublunatum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'mol_type="genomic DNA"
'strain="BBA62431"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Fusarium sublunatum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="ITS1"
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Pred. No. 3.3e+02;
0; Mismatches 1;
                                                                                 Wingfield, B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spacer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              var. sublunatum"
                                                                                   Marasas, W.F.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 419;
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                                                                                                                                                                                                                                           Fusarium.
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SOURCE
ORGANISM
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JOURNAL
Query Match
Best Local Similarity
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Best Local :
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-OCT-2001) Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Lunnonstreet, Pretoria, Gauteng 0002, South Africa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 421)
Britz,H., Coutinho,T.A.,
Wingfield,M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Britz,H., Coutinho,T.A., Wingfield,B.D., Marasas,W.F.O. and Wingfield,M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF430129 PIN 06-1 PIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vegetative compatibility and distribution of two Fusarium species associated with mango malformation in South Africa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusarium mangiferae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusarium mangiferae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTAGTGACGGTCTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Fusarium mangiferae"
/mol_type="genomic DNA"
/strain="MRC7035"
                                                                                                                              /product="internal transcribed
                                                                                                                                                                                             product="5.8S ribosomal RNA"
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                                                                                                                                                                                                                                                                                                                        product="18S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                           note="section Liseola"
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/strain="MRC3477"
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                                                                                                                                                                                                                                                                                                 . 161
   91.1%;
94.4%;
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94.4%;
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   Score 16.4; DB 8; Pred. No. 3.3e+02;
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Pred. No. 3:3e+02;
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                                 Length 421;
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AUTHORS
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
AF502877
LOCUS
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VERSION
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VERSION
KEYWORDS
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DEFINITION
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Best Local S
Matches 17
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JOURNAL
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                                                                                                                                                                                                                                                                                  387
                                                                                                                                      Ascomycete sp. A77 internal transcribed spacer 1, partial 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

AX243055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leaf litter ascomycete strain its389
leaf litter ascomycete strain its389
Eukaryota; Fungi; Ascomycota.
1 (bases 1 to 427)
Gilbert, G.S., Garbelotto, M., Chapela, I., Moeller, C. and Dreyfuss, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
AF502877
             ascomycete sp. A77
ascomycete sp. A77
Eukaryota; Fungi; Ascomycota.
1 (bases 1 to 434)
Beckstad, J. and Parker, I.M.
Invasiveness of Ammophila arenaria:
                                                                                                                                                                                                                                                                                                                                                 Similarity 94.4
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 427)
Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C.
Dreyfuss,M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biogeography of leaf litter fungi
Unpublished
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A27 bp DNA linear PLN 13-MAY-2002 leaf litter ascomycete strain its389 isolate 1000096987 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="5.8S ribosomal RNA" 320. .>427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="internal transcribed spacer 1" 165. .319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /isolate="1000096987"
/specific_host="Prestoea montana"
/db_xref="taxon:194149"
/country="Puerto Rico"
                                                                                                                                                                                                                                                                                                                                                                                                                             /product="internal transcribed spacer 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="leaf litter ascomycete strain its389"
/mol_type="genomic DNA"
/strain="its389"
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94.48;
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/db_xref="taxon:227269"
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/mol_type="genomic DNA"
/strain="A77"
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Aaq62632 Porphyrin	Abs11282 Human gen	Abs36962 Human liv	Aakl1513 Human bra	Aak37292 Human bon	Aba30343 Probe #88	Aai43123 Probe #11	Aba63091 Human foe	Probe	Aba08494 Human Fc-	Abs23648 Human gen	Abs49806 Human liv	Aak24114 Human bra	Aak50175 Human bon	Aba40157 Probe #18	Aai56113 Probe #24	Aba75543 Human foe	Aai27255 Probe #17	Aaq54386 T. niveum	٠	Aah54021 S. epider	Aah53831 S. epider

ALIGNMENTS

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RESULT 1
AAV83696
Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxil; M. racemosus; M. plumbeus; M. indicus; A. fumigatus; M. microsporus; M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus; R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum; Penicillium notatum; Sporothrix schenkii; filamentous fungus; ss.
                                     New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothr
                                                                                              WPI; 1999-034737/03.
                                                                                                                        Morrison
                                                                                                                                                                               02-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                               Synthetic.
Gibberella fujikuroi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species-specific probe targeted to the internal transcribed spacer
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/note= "labelled with digoxigenin"
                                                                                                                        Aidorevich L, Choi JS;
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                                        Sporothrix
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ABK84699 ABN97319 AAI74530 AAI74531

Example 1; Page 22; 45pp; English

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A. terreus; M. racemosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probes AAV83677-708 are derived from the internal transcribed spacer 2 (ITS2) region of various filamentous fungi (see AAV70845-73). The probes are species-specific, and can be used for identifying a species selected from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans, F. searnium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus, M. circinialloides f. circinelloides, Rhizopus oryzae, R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallesheria boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenkii. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi
                                                                                                                                                                         Aspergillus, Fur
Cunninghamella,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus; R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum; Penicillium notatum; Sporothrix schenkii; filamentous fungus; ss.
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26-FEB-1999
                                                                                                                                                                                                                                                                                                                                       02-MAY-1997;
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                                                                                                                                                                                                          New nucleic acid probes
                                                                                                                                                                                                                                           WPI; 1999-034737/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; racemosus; M. plumbeus; M. indicus; A. fumigatus; circinilloides f. circinelloides; Rhizopus orvzae. p -:- circinans; R. stolonifer. ph:---
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                                                                                                                                                                         acid probes for filamentous fungi - for detecting e.g.
Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
la, Pseudoallescheria boydii, Penicillium and Sporothr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ITS2) and adjacent regions.
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The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species-specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans, Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeu M. indicus, M. circinilloides f. circinelloides, Rhizopus oryzae, R.

Claim 1; Page 12; 45pp;

English.

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RESULT 3
ADA61893
ADA
The invention relates to novel steroid compounds derived from the African soil fungus Fusarium sp. WF6381 (ATCC 7449) which act as inhibitors of HIV integrase. The invention encompasses cultures of Fusarium sp. MF6381. The invention also relates to a composition comprising a compound of the invention in combination with an AIDS antiviral agent, an immunomodulator and an antiinfective agent. The compounds of the invention may be used in the inhibition of HIV integrase and in the prevention and treatment of HIV infection. A wide range of state of HIV infection may be treated:

AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex); but a cquired immunodeficiency syndrome); ARC (AIDS-related complex); compounds which are potentially useful as screening tools for antiviral compounds. The compounds may be used to isolate HIV integrase compounds. The compounds may also be used to establish or determine the site at which other antivirals bind to HIV integrase (e.g., by competitive inhibition). The present sequence represents the ribosomal DNA (rDNA) internal transcribed spacer (ITS) region of Fusarium sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 14; 113pp; English
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14-NOV-2000
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                                                                                                                                                                         This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods and primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present
                                                                                                                                                                                                                                         Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
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 14-JAN-2003
                  ABV78700;
                                   ABV78700 standard;
                                                                                                                                                  Sequence 534 BP; 135 A; 149 C; 130 G;
                                                                                                                                                                    sequence represents an internal transcribed spacer RNA encoding
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                                                                                                                                                                                                                                                                                                        Beck JJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondria; fungal pathogen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Internal transcribed spacer RNA encoding
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Pred. No. 43
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel base sequence which is part of a fully defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispora. The base sequences can be used for the classification of Cordyceps sinensis. The sequence represents a C. crassispora rRNA sequence of the
                                                             misc_feature
                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fungus genomic DNA spanning 18S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HEAL-) HEALTHWAY KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  crassispora rRNA sequence
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1 Similarity 94.48;
17; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               control; fungus;
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                                                      /note= "5.8S;
2079. .2347
                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
   note=
                                                                                                                                                                 /note= "ITS1 region"
1922. .2078
                                                                                                                                                                                                                                                                                                   note= "18S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
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"ITS2 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2293
                                                                                                                                                                                                                                                                                            rRNA gene"
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Pred. No. 44
                                                                                                rRNA gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.8S and 28S rRNA and ITS sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 647;
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RESULT 7

AAC42796
ID AAC4
XX AAC4
XX AAC4
XX Arab
XX Hybx
XX Hybx
XX Hybx
XX Prom
XX Prom
XX Arab
XX 
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a genomic DNA sequence containing the 18S rRNA gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S rRNA sequences from a mutant strain of Gibberella fukkkoroi (LTB-1027) of the invention. This region of DNA is highly variable and can be used for species and strain differentiation. The LTB-1027 mutant produces a mixture of gibberellins which is at least 70 % GA 4 and GA 7. Gibberellins GA_4 and GA_7 promote flowering and Fruit cell elongation, and are used by growers of apples, pears and grapes to produce larger fruits and earlier harvests. The mixture of GA_3, GA_4 and GA_7 achieved using the method of this invention should be particularly useful in the apple industry where GA_4 has been found more effective in russet control and in promoting fruit set. This method produces GA_4 and GA_7 in much higher titers than prior art methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A new method for producing a mixture of gibberellins from Giberella fujikuroi results in high titers of GA4 and GA7 useful to promote flowering and fruit growth in the fruit growing industry.
                                                                                                                                                                                                        Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway;
   25-FEB-1999;
                                     25-FEB-2000; 2000EP-00301439.
                                                                            06-SEP-2000.
                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                           promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                    Arabidopsis thaliana DNA fragment SEQ ID NO: 36883.
                                                                                                                                                                                                                                                                                                           17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                AAC42796;
                                                                                                                                                                                                                                                                                                                                                                                  AAC42796 standard; DNA; 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Col 9-12; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallazzo JL, Lee MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-2000; 2000US-00645073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GALL/) GALLAZZO J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2145 TCTAGTGGCGGTCTCGCT 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                         (first
   99US-0121825P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0151770P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= e
/note= "28S rRNA gene"
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                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.1%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                  BP
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Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
21-MAY-1999;
25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

06-APR-1999

06-APR-1999

16-APR-1999

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23-APR-1999

23-APR-1999

23-APR-1999

06-MAY-1999

06-MAY-1999

06-MAY-1999

06-MAY-1999

07-MAY-1999

07-MAY-1999

07-MAY-1999

07-MAY-1999

07-MAY-1999
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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
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               99US-0130449P

99US-0130410P

99US-0131449P

99US-0132484P

99US-0132484P

99US-0132486P

99US-0134218P

99US-0134256P

99US-0134256P

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99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-0126745P.
99US-0127462P.
99US-0128234P.
99US-0128234P.
99US-0128234P.
99US-0128774P.
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RESULT 8
ACH46296/c
ID ACH46296 E
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ACH46296;
AC
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Best Local S
Matches 16
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07-0CT-1999

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21-0CT-1999
                                                                                                                                                                                                                                                            US2003073623-A1.
                                                                                                                                                  30-JUL-2001; 2001US-00918995
                                                                                                                                                                                       30-JUL-2001;
                                                                                                                                                                                                                            17-APR-2003
                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                  13-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218
                                                                                                                                                                                                                                                                                                                                                                                               infant brain
                                 ) DRMANAC R T.
) LABAT I.
) STACHE-CRAIN I
) DICKSON M C.
) JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                      ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
 RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTAGTGACGGTCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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 Labat I,
                                                                                                                                                                                       2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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99US-0158029P

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99US-0159294P

99US-0159293P

99US-0159231P

99US-0159331P

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99US-0159638P

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99US-0160814P

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99US-0161405P

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99US-0161359P

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                                                                                                                                                                                                                                                                                                                                                                                             CDNA #359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA;
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94.1%;
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 Stache-Crain
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Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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   Dickson
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 MC,
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   Jones
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20-AUG-1999
20-AUG-1999
20-AUG-1999
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99US-0143624P99US-0144086P99US-0144331P99US-0144331P99US-0144331P99US-0144331P99US-0144331P99US-0144331P99US-0144331P99US-0144331P99US-0144331P99US-0144884P99US-0145088P99US-014508P99US-014508P99US-0145145P99US-0145145P99US-0145145P99US-0145145P99US-0145145P99US-014638P99US-014591P99US-014591P99US-014591P99US-014731P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-0147303P99US-014972P99US-014972P99US-014973P99US-0151066P99US-0151068P99US-015303P99US-015303P99US-015303P99US-015403P99US-015403P99US-015548P99US-0155659P99US-015659P99US-015659P99US-015659P99US-015659P-

New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating

Claim 1;

SEQ ID NO 33508; 44pp; English

antisense DNA or RNA.

2003-615964/58

The invention relates to an isolated polynucleotide comprising any one of CC 38043 cDNA sequences, appearing as ACHI-2789-ACH50831, whose sequence was CC determined by the technique of SBH (sequencing by hybridisation). Also CC included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences CC are useful in diagnostics as expressed sequence tags (EST) for CC identifying expressed genes or for physical mapping of the human genome, CC in forensics, in assessing biodiversities, or in identifying mutations CC responsible for genetic disorders and other traits. The nucleotide CC sequences are also useful as hybridisation probes, as oligomers for PCR, CC protein, or in generating antisense DNA or RNA. The purified polypeptide cis useful for generating antisense DNA or RNA. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data CC for this patent did not form part of the printed specification, but was compared to the compared the compared to the compared to

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4

AGTGACGGTCTCGCT 18

Query Match Best Local S Matches 15

l Similarity

Conservative

<u>;</u>

Mismatches

2.5e+02; hes 0; DB 8;

0,

Gaps

0;

Length 386; Indels

83.3%; 100.0%;

Score 15; pred. No.

Sequence 386

seqdata.uspto.gov/sequence.html?DocID=20030073623

BP; 101 A; 105 C; 116 G; 64 T; 0 U; 0 Other;

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RESULT 9
ADC30089/c

ID ADC30089;

XX
AC ADC30089;

XX
T 18-DEC-2003 (first entry)

XX
Human novel cDNA sequence, SEQ
XX
Human novel cDNA sequence, SEQ
XX
Human; diagnostic; drug screen:
KW biodiversity assessment; Parkin

XW neurodegenerative diseases; and
XW neuroprotective; antianaemic; id

KW neuroprotective; antianaemic; id

KW neuroprotective; antianaemic; id

XX
M neuroprotective; antianaemic; id

XX
N antiulcer; osteopathic; immuno;

XX
N antiulcer; osteopathic; im
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemic, pattelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy; chromosome 6p21.3; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTGACGGTCTCGCT
              J, Ren F, Xt, Wang D, Mang D, Mang D, Mang D, Mang D, Mang Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:171.
                                                                Xue AJ, Zhao QA,
Ma Y, Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽₽
                                                                Wang J,
Wang Z,
                                                                     Weng
                                                                                                                  Wehrman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic;
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CC ADC30889) and the polypeptides they encode (ADC3080-ADC3180). The clivention also relates to nucleic acid sequences over 99% identical with CC invention also relates to nucleic acid sequences over 99% identical with CC the novel human cDNAs. The invention additionally encompasses expression convectors and host cells comprising a nucleic acid of the invention; the creambinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an entibody CC against a polypeptide of the invention; and methods of polynucleotides or polypeptides of the invention; and methods of and/or monoclonal antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the cappression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention are cuseful in diagnostics, drug screening, forensics, gene mapping, in the CC data and products dependent on DNA and amino acid sequences. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer and in the recombinant production of a protein. The polypeptides of this patent did not form part of the printed specification, but was cobtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide and polypeptide useful for diagnosing, preventing of treating conditions such as neurodegenerative diseases, anemias, plated disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-371981/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 171; 1185pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 platelet
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Query Match Best Local (Matches Sequence 432 BP; 118 A; 113 C; 123 G; 123 4 AGTGACGGTCTCGCT 18 Similarity AGTGACGGTCTCGCT Conservative 83.3%; 109 Score 15; ; Pred. No. 0 Mismatches DB 9; uc.. o. 2.5e+02; 0; 78 T; 0 U; 0 Other; Length 432; Indels 0 Gaps

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RESULT 10
ACH47075/c
ID ACH470
XX
ACH470
AC ACH470
XT
I3-OCT
XX
Human
XX
Human;
KW Human;
KW genome
XX
Homo s
XX
PN US2003
XX
PD 17-APR
                                                                     Human;
genome
                                                                                                      Human infant brain cDNA #1138
                                                                                                                            13-OCT-2003
                                                                                                                                                                        ACH47075 standard; cDNA; 449
                          US2003073623-A1
                                               Homo sapiens
                                                                              88;
                                                                     mapping;
                                                                     sequencing by hybridisation; SBH; expressed ping; biodiversity; genetic disorder.
                                                                                                                            (first
                                                                                                                            entry)
                                                                                                                                                                           ВP
                                                                                  sequence tag;
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RESULT 11
ACH13812/c
ID ACH13812 standard; cDNA; 473 BP
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antiseense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for
                                                                                                                                   genome
30-JUL-2001; 2001US-00918995
                         30-JUL-2001; 2001US-00918995
                                                      17-APR-2003
                                                                               US2003073623-A1
                                                                                                         Homo sapiens
                                                                                                                                                                          Human adult brain cDNA #1024.
                                                                                                                                                                                                      13-OCT-2003
                                                                                                                                                                                                                                 ACH13812;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 34287; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide sequences obtained from various as hybridization probes, as oligomers for PCR, for mapping, in the recombinant production of protein, antisense DNA or RNA.
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(STAC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                253
                                                                                                                                 ss; sequencing by hybridisation;
mapping; biodiversity; genetic d;
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                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
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LABAT I.
STACHE-CRAIN I
DICKSON M C.
JONES L W.
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                                                                                                                                                                                                                                                                                                                                                AGTGACGGTCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                          449
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                                                                                                                                                                                                                                                                                                                                                                                   Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                          BP;
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                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          118
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; 124 C; 127
                                                                                                                                                                                                                                                                                                                                                                                                              83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                    n; SBH; ex
disorder
                                                                                                                                                                                                                                                                                                                                                                              DB 8; L-
3. 2.5e+02;
0;
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                                                                                                                                              expressed
                                                                                                                                                                                                                                                                                                                                                                                                            Length 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA libraries, useful chromosome and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones
                                                                                                                                               sequence tag; EST;
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RESULT 12
AAT99147/c
ID AAT991
XX AAT991
XX AAT991
XX S-aden
XX S-
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in telectronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                           S-adenosylmethionine synthase 2 gene; barley; alkali resistant plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT99142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT99142 standard; cDNA to mRNA; 1182 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide sequences obtained is hybridization probes, as oligomers is mapping, in the recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LABA/)
(STAC/)
(DICK/)
                                                                                                                                                      28-MAY-1996;
                                                                                                                                                                                                            09-DEC-1997.
                                                                                                                                                                                                                                                                                                              Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seqdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated polynucleotide comprising any one 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence watermined by the technique of SBH (sequencing by hybridisation). Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1024; 44pp; English.
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                                                   (NIOC ) NIPPON OIL CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JONE/)
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LABAT I.
STACHE-CRAIN
DICKSON M C.
JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTGACGGTCTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                    96JP-00133406
                                                                                                                                                      96JP-00133406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 A; 121 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               synthase 2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 G; 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for PCR, for of protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8; Le 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA libraries,
chromosome and c
or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones
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was 2

WPI; 1998-080077/08

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RESULT 13
AASB8320
ID AASB8
AC AASB8
AC
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Best Local (
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                         sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore mormal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The
                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-adenosyl-methionine synthase gene - useful in producing plants resistant to alkaline soil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                             1; SEQ ID NO 24124; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        novel human diagnostic protein #24124.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder; ss.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ç;
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o. 2.7e+02;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; bur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printled specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                    molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antilicer; osteopathic; immunosuppressive; antiinflammatory; cytostati
                                                                                                                                                                                                                                                                                  24-SEP-2001; 2001US-0324631P
                                                                                                                                                                                                                                                                                                       24-SEP-2002; 2002WO-US030474.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ulcers; osteoporosis; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human novel cDNA contig sequence, SEQ ID NO:2090.
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Ghosh M,
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Drmanac R'
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Pred. No.
                                                                                                                                                                                                                         AJ, Zhao QA,
Y, Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              462 G;
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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; a method of detecting polynucleotides or polypeptides of the invention; and methods of

New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

2003-371981/35. DB; ADC32775.

Example 2; SEQ

ID NO 2090; 1185pp; English.

markers that is useful for monitoring disease states and drug toxicity.

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ABK84372
ID ABK844372
ID ABK844XX
AC ABK84
AC AB
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; 88; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-2001; 2001WO-US030821.
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                                                                                                                                    WPI; 2002-435328/46.
                                                                                                                                                                                                                     Beazer-Barclay Y,
                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2000; 2000US-0237189P
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                                                                                                                                                                                                                                                                                                               (GENE-) GENE LOGIC INC.
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                                                                                                                                                                                                                     Weissman SM,
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100.0%; Pred. No.
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                                                                                                                                                                                                                     Vockley J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>.</u>
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묽 5

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ftp.wipo.int/pub/published_pct_sequences
                                      Claim 1; SEQ ID NO 943; 114pp; English
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37160 BP; 10453 A; 8097 C; 8175 G; 10435 T; 0 U; 0 Other;

Query Match Local l Similarity Conservative 100.0%; 83.3%; 0 Score 15; Pred. No. Mismatches DB 6; Le Length 37160; <u>.</u> Gaps

0

Search completed: October time 38.9347 ļ, 2004, 03:41:10

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic

Mis Page Blank (Uspto)

43

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Copyright
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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OM nucleic nucleic search, using sw model

Title: Run on: October 1, 2004, 03:09:43; Search time 5.93182 Seconds (without alignments) 1683.989 Million cell updates/sec

Sequence: Perfect score: US-10-046-955-49 18 tctagtgacggtctcgct 18

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Maximum Minimum DB seq length: 0 DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Result No.
11111111111111111111111111111111111111	Score
100.0 91.1 91.1 91.1 91.1 91.7 91.7 91.7 91.7	Query
18 310 583 594 2293 531 531 1908 46899 636 636 636 636 636 637 777 777 777 777	Length
4 4 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	BB
US-09-423-233-49 US-08-652-127C-8 US-08-652-127C-8 US-08-652-127C-5 US-08-652-127C-7 US-08-652-127C-7 US-08-652-127C-6 US-09-645-073-1 US-08-652-127C-6 US-08-652-127C-6 US-08-652-127C-6 US-08-737-129A-1 US-08-737-129A-1 US-08-737-129A-1 US-08-737-129A-1 US-08-737-129A-5 US-08-737-129A-5 US-08-737-129A-5 US-08-737-129A-5 US-08-737-129A-5 US-08-737-129A-5 US-08-867-86A-65 PCT-US94-14106-54 US-08-867-86A-65 US-08-133-011-99 US-08-133-011-99 US-08-383-613-99 US-08-133-011-115	ID
Sequence 49, Appli Sequence 7, Appli Sequence 8, Appli Sequence 1, Appli Sequence 7, Appli Sequence 6, Appli Sequence 1914, Ap Sequence 1914, Ap Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 58, Appli Sequence 58, Appli Sequence 50, Appli Sequence 52, Appli Sequence 53, Appli Sequence 54, Appli Sequence 59, Appli Sequence 99, Appli Sequence 91, Appli	Description

Best Local Similarity Matches 17; Conserv

Conservative

0; Mismatches Score 16.4; DI Pred. No. 6.3;

1:

Indels

0;

Gaps

0

91.1%; 94.4%;

₽B 4.

Length 310;

Query Match

14 77.8 830 1 US-08-322-730A-115 14 77.8 830 1 US-08-387-874-88 14 77.8 830 2 US-08-383-619-115 14 77.8 830 3 US-08-907-739-115 14 77.8 830 4 US-09-729-597-115 14 77.8 830 5 PCT-US93-08364-88 14 77.8 830 5 PCT-US93-08364-88 14 77.8 1077 4 US-09-489-039A-1514 14 77.8 1147 6 5455030-2 853-19 14 77.8 1144 3 US-08-403-853-19 14 77.8 1446 3 US-08-171-945-130 14 77.8 1641 2 US-08-353-400-23 14 77.8 1642 2 US-08-792-824-8 14 77.8 1672 2 US-08-792-824-2 14 77.8 1679 3 US-08-792-824-2 14 77.8 1797 3 US-08-792-824-2 17 77.8 1797 3 US-08-792-824-2 17 77.8 1797 3 US-08-792-824-2 17 77.8 1797 3 US-08-792-824-2
1077 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1 1 2 2 2 4 7 8 4 8 8 4 8 4 8 8 4 8 8 8 8 8 8 8 8
1 US-08-322-730A-115 1 US-08-387-874-88 2 US-08-387-874-88 2 US-08-907-739-115 3 US-08-907-739-115 4 US-09-729-597-115 5 PCT-US93-08364-88 5 PCT-US93-08364-88 6 PCT-US93-0859-1 4 US-09-489-039A-1514 6 5455030-2 8 US-08-403-253-19 9 US-08-403-253-19 1 US-08-353-400-23 1 US-08-353-400-23 2 US-08-792-824-8 2 US-08-792-824-8 2 US-08-792-824-2 1 US-08-792-824-2 2 US-08-792-824-2
US-08-387-874-88 US-08-387-874-88 US-08-383-619-115 US-08-297-739-115 US-08-729-597-115 US-09-729-597-115 PCT-US93-08364-88 PCT-US93-08364-88 PCT-US93-08364-88 PCT-US93-08364-89 US-08-403-853-19 US-08-403-853-19 US-08-403-853-19 US-08-403-853-400-23 US-08-792-824-8 US-08-792-824-2 US-08-792-824-2 US-08-792-824-2 US-08-792-824-2 US-08-792-824-2 US-08-792-824-2 US-08-792-824-2 US-08-792-824-2 US-08-792-824-2 US-08-792-940-6

ALIGNMENTS

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RESULT 2
US-09-423-233-7
US-09-423-233-7
; Sequence 7, Application US/09423233
; Patent No. 6372430
; Patent No. 6372430
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-09-423-233-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-09-423-233-49
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                                                                                                GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILLNG DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as ITILE OF INVENTION: Nucleic Acids for Detecting Aspergillus STITLE OF INVENTION: Other Filamentous Fungi FILE REFERENCE: 03063-0341WP CURRENT APPLICATION NUMBER: US/09/423,233 CURRENT FILING DATE: 2000-06-27 NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 49
LENGTH: 18
                                                                                     SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 49, Application US/09423233 Patent No. 6372430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 18;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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TCTAGTGGCGGTCTCGCT 191 TCTAGTGACGGTCTCGCT

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                                                                                                                                                                         Sequence 5, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF
TITLE OF INVENTION: PATHOGEN FUNC
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08652127C Patent No. 5792611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (613) 232-5831 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Richar
                                      STREET: butawa CITY: Ottawa Canada
                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DETECTION OF P.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
                              COUNTRY: Cana
ZIP: K1R 6K7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                     ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby & MacLean
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby & MacLean
STREET: 880 Wellington Street, Suite 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                     91.1%;
il Similarity 94.4%;
17; Conservativa
                                                                                                                                                                                                                                                                                                                                                                         1 TCTAGTGACGGTCTCGCT 18
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                                                                                                                                                                                                                                                                                                                                                     TCTAGTGGCGGTCTCGCT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   583
                                                                                   880 Wellington Street, Suite 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Richard C. Hamelin
PENTION: DETECTION OF PLANT
                                                                                                                                                                          DETECTION OF PLANT PATHOGEN FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1898
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.4;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Sequence 7, Application US/08652127C Patent No. 5792611

GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS

George A. Seaby Seaby & MacLean

```
GENERAL INFORMATION:
APPLICANT: Lee, May
APPLICANT: Lee, May
APPLICANT: Galazzo, Jorge
ITILE OF INVENTION: Production of High Tit
FILE REFERENCE: L02-0LNP
CURRENT APPLICATION NUMBER: US/09/645,073
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,770
PRIOR FILING DATE: 1999-08-31
                                                                                                                 Query Match
Best Local Similarity
Watches 17; Conserve
US-08-652-127C-7
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                                                                                               Ś
                                                                                                                                                                                                   ; ORGANISM: Gibberella fujikuroi US-09-645-073-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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               RESULT 6
                                                                                                                                                                                                                                              ; SOFTWARE: Pal
; SEQ ID NO 1
; LENGTH: 2293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-09-645-073-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-652-127C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: GEOTGE A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5831
TELEPAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09645073 Patent No. 6287800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 91.3
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: May 23, 199
CLASSIFICATION: 435
                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                    2145 TCTAGTGGCGGTCTCGCT 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439 TCTAGTGGCGGTCTCGCT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TCTAGTGACGGTCTCGCT 18
                                                                                        TCTAGTGACGGTCTCGCT 18
                                                                                                                                                                                                                                                                                     PatentIn version 3.0
                                                                                                                                  Conservative
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             May 23, 1996
                                                                                                                                                                                                                                                                                                                                                                                                      Production of High Titers of Gibberellins GA4 and GA7
                                                                                                                                                  91.1%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.18;
94.48;
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                                                                                                                                  <u>,</u>
                                                                                                                                                  Score 16.4; D
Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.4;
Pred. No. 6
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                                                                                                                                    Mismatches
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                                                                                                                                                                  Length 2293;
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                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear US-08-652-127C-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08652127C Patent No. 5792611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
                                                TELEPHONE: (613) 232-5815
TELEPAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (613) 232-5831 INFORMATION FOR SEQ ID NO: 7:
                                                                            NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DETECTION OF PLANT TITLE OF INVENTION: PATHOGEN FUNGI NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
           SEQUENCE CHARACTERISTICS:
LENGTH: 581
                                                                                                                                                                       APPLICATION NUMBER: US/08/652,127C FILING DATE: May 23, 1996 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                           SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-D
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                      STREET: 880 W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: K1R 6K7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 880 GCITY: Ottawa
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby & MacLean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 TATAGTGGCGGTCTCGCT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                         K1R 6K7
nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                         880 Wellington Street, Suite 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Richard C. Hamelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                      1898
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Pred. No. 49;
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2042
LENGTH: 1629
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; STRANDEDNESS: ; TOPOLOGY: lin US-08-652-127C-6
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US-09-252-991A-1914/c
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US-09-252-991A-2042
                                                                                                                                            APPLICATION NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ACID SEQUENCES AND THERAPEUTICS

FILE REFERENCE: 107196.136

FULL REFERENCE: 107196.136

CURRENT FILING NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NO 1914

LENGTH: 1908

TYPE: DNA

TYPE: DNA

FORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1914, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2042, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                    Best Local Similarity
Matches 15; Conserv
                                                                                                        Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
1286 TACTGACGGTCTCGCT 1271
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                                  TAGTGACGGTCTCGCT 18
                                                                      Conservative
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93.8%;
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93.8%;
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                                                                                       Score 14.4;
Pred. No. 91
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Pred. No. 8
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Pred. No. 4
                                                                        Mismatches
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                                                                                                        Length 1908;
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RESULT 11
US-08-737-129A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kassenoff, Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 100-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 84/4
TELEPAX: 201 503 8807
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                 Sequence 1, Application US/08737129A Patent No. 5885816 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              Matches
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COMPUTER READBLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/471,119A
STREET: bull
CITY: Washington
STATE: D.C.
                                                                                     APPLICANT: Ikuo FUJII et al.
TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tolypocladium niveum
STRAIN: ATCC 34921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schneider, Elisabeth APPLICANT: Schoergendorfer, Kurt APPLICANT: Weber, Gerhard TITLE OF INVENTION: Cyclosporin S NUMBER OF SEQUENCES: 8
                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Leitner, Ernst
APPLICANT: Schneider, Elisabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DI
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STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                    15595 CTGGTGACGGTCTCGC 15610
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US-09-170-769A-1
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US-09-170-769A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
APPLICANT: LETURCO, Didier
APPLICANT: MORIATRY, Ann
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09170769A Patent No. 6444206
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Best Local Similarity
Matches 14; Conserv
                                                                      Query Match
Best Local Similarity
                                                                                                                                            ORGANISM: Murine FEATURE: NAME/KEY: CDS LOCATION: (1)..(639)
                                                                                                                                                                                                                                                                                                                                         APPLICANT: TOBIAS, Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVATIONER REFERENCE: SCRIP1140-3
CURRENT APPLICATION NUMBER: US/09/170,769A
CURRENT FILING DATE: 1998-10-13
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 08/070,160 PRIOR FILING DATE: 1993-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 636 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY AGENT INFORMATION:
ATTORNEY WATTER M. Cheek, Jr.
NAME: WATTER M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOTOGETFECT 5.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/6
FILING DATE: NO. 5885816
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                       ENGTH: 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               566 GTGACGGTCTCGCT 553
                                                      14;
5 GTGACGGTCTCGCT 18
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MORIATRY, Ann
ULEVITCH, Richard
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                                                      Conservative
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                                                                      100.0%;
                                                                                          77.8%;
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                                                                         Score 14; DB 4; ; Pred. No. 1.4e+
                                                        Mismatches
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                                                                         1.4e+02;
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                                                                                       Length 639;
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                                                        Indels
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RESULT 14
US-08-737-129A-5/c
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US-09-170-769A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-170-769A-5/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09170769A Patent No. 6444206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TOBIAS, Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
FILE REFERENCE: SCRIP1140-3
CURRENT APPLICATION NUMBER: US/09/170,769A
CURRENT FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/070,160
PRIOR APPLICATION NUMBER: US 08/070,160
PRIOR PILING DATE: 1993-05-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: THE SCRIPPS RESEARCH INSTITUTE APPLICANT: LETURCQ, Didier APPLICANT: MORIATRY, Ann APPLICANT: ULEVITCH, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ikuo F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Murine
             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                 APPLICATION NUMBER: US/08/737,129A
FILING DATE: No. 5885816ember 15, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 645
                                                                                                                                                                                                             SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ikuo FUJII et al.
TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                     STREET: 805 Fifte
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  596 GTGACGGTCTCGCT 583
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Similarity 100.0%; Pred. No. 1.4e+0
14; Conservative 0; Mismatches
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805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                     Diskette,
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Search completed: October Job time: 7.93182 secs

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2004, 08:05:42

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RESULT 15
PCT-US94-14106-58/c
; Sequence 58, Application PC/TUS9414106
; GENERAL INFORMATION:
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                                                                                                             PCT-US94-14106-58
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                                                       Matches
                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                     FEATURE:
                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Process for Generating Specific Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MODIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US94/14106 FILING DATE:
                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 666 bases
653 GTGACGGTCTCGCT 640
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                                                     14;
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                          GTGACGGTCTCGCT 18
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                                                     Conservative
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67..717
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100.0%;
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                                                    Score 14; DB 5; ; Pred. No. 1.4e+02 0; Mismatches 0
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18-10-040-933-43
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM nucleic - nucleic search, using sw model
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Pred. No.
                                     Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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19: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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Gapop 10.0 , Gapext 1.0
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18
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Search time 73.304 Seconds (without alignments) 1244.847 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

13 14	110		ი ი თ თ	0 سي	21	Result No.
14.8 14.8	14. 888	14.8	15 15	16.4 15	18	Score
82.2 82.2	82.2 82.2	B2.2 82.2	83.3 83.3	91.1 83.3	100.0	Query Match
675 3461	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	558 558	449 473	534 386	310	Length
17 17	13 16	13	10	10	15	DB
US-10-767-701-8208 ' US-10-437-963-82321	US-10-027-632-215234 US-10-027-632-215235 US-10-027-632-215234 US-10-027-632-215235	US-10-424-599-44516 US-10-437-963-74582	US-09-918-995-34287 US-09-918-995-1024	US-09-961-755A-7 US-09-918-995-33508	US-10-046-955-49 US-10-046-955-7	ID
	Sequence 215234, Sequence 215235, Sequence 215234, Sequence 215235,	Sequence 44516, A Sequence 74582, A	Sequence 34287, A Sequence 1024, Ap	Sequence 7, Appli Sequence 33508, A	Sequence 49, Appli Sequence 7, Appli	Description

C 45	C 44		c 42	C 41		c 39		c 37			c 34			c 31			c 28			c 25	c 24	c 23	22	c 21	20	19	18	17	16	15
14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14.8	14.8	14.8	14.8	14.8
77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8		77.8	77.8	77.8	77.8		77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	'n		2	82.2	82.2
1707	1701	1671	1636	1516	1446	1445	1398	1386	1386	1383	1383	1371	1353	1314	1056	830	798	741	736	672	666	613	550	489	479	198285	198285	75839	60500	28573
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US-09-815-837-64	US-09-815-837-62	US-10-679-620-85	US-10-767-701-13810	US-09-903-327A-1	US-09-910-059-130	US-10-679-620-71	US-10-275-180A-21	US-10-286-132A-21	US-10-281-479A-21	US-10-719-642-96	US-10-719-642-95	US-10-719-642-82	US-10-679-620-77	US-09-903-327A-5	US-10-134-188-30	US-10-273-973-115	US-10-273-973-99	US-10-251-215-48	US-10-006-773-12	US-10-410-907A-35	US-10-679-620-81	US-10-767-701-24494	US-09-864-761-8809	US-10-276-774-270	US-09-864-761-25477	US-10-775-169-338	US-09-880-107-3814	US-10-087-192-166	US-10-087-192-1024	US-10-741-601-5769
Sequence 64, Appl	Sequence 62, Appl	Sequence 85, Appl	Sequence 13810, A	Sequence 1, Appli		•	-	21,	21,	Sequence 96, Appl	95,	82,	Sequence 77, Appl	Sequence 5, Appli		115,			12,	Sequence 35, Appl	81,	94	Sequence 8809, Ap	Sequence 270, App	25477,	Sequence 338, App	Sequence 3814, Ap	166, 1	*	Sequence 5769, Ap

ALIGNMENTS

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; TYPE: DNA ; ORGANISM: Fusarium moniliforme US-10-046-955-49
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US-10-046-955-49
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Publication No. US20030129600A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dise APPLICANT: Control and Prevention

APPLICANT: Morrison, Christine J.

APPLICANT: Reiss, Errol
                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 49
LENGTH: 18
                                                                              Matches
                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                              APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER: OF SEQ. ID NOS: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                              18;
TCTAGTGACGGTCTCGCT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aidorevich,
                                                                    100.0%; Score 18; DB liarity 100.0%; Pred. No. 8.4; Conservative 0; Mismatches
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                                                                                                                         DB 15; Length 18;
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                                                                                                                                                  LENGTH: 534
TYPE: DNA
CORGANISM: Fusarium proliferatum
US-09-961-755A-7
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US-09-961-755A-7
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CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Beck, Jim
APPLICANT: Beck, Jim
APPLICANT: Bernett, Jason
TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 66055
CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/10046955
Publication No. US20030129600A1
                                                                                                                                                                                                                             SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09961755A Publication No. US20030113722A1
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                                                                           Matches
                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: The Government of the United States of APPLICANT: Secretary of the Department of Health APPLICANT: Control and Prevention
                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Fusarium moniliforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                          Local
402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.1%;
11 Similarity 94.4%;
17; Conservative
                                                                           l Similarity
17; Conserv
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                                     TCTAGTGACGGTCTCGCT 18
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TCTAGTGGCGGTCTCGCT 419
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                                                                           Conservative
                                                                                        91.1%;
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                                                                         Score 16.4; D
Pred. No. 55;
0; Mismatches
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Pred. No. 5
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                                                                                                              DB 10;
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                                                                                                            Length 534;
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RESULT 4

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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
FRIOR APPLICATION NUMBER: US/09/235,076
PRIOR REPLICATION NUMBER: US/09/235,076
PRIOR RETLING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FBESSEQ for Windows Version 3.0
SEQ ID NO 33508
LENGTH: 386
TYPE: DNA
CENTRAL CONTRAL CONTR
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                                                                                                                                                                                                                                                                                                                      RESULT 6
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US-09-918-995-34287/c
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33508, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
                          GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 34287
                                                                                                                                                                                                                Sequence 1024, Application US/09918995 Publication No. US20030073623A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756 CURRENT APPLICATION NUMBER: US/09/918,995 CURRENT FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: US/09/235,076 PRIOR RILICATION NUMBER: US/09/235,076 PRIOR FILING DATE: 1999-01-20
CURRENT APPLICATION NUMBER: US/09/918,995
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LOCATION: (1)...(449)
OTHER INFORMATION: n = A,T,C or G
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1024
LENGTH: 473
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                      GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey F
                                                                                                                                                                                                                                                                             RESULT 8
US-10-437-963-74582/c
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OTHER INFORMATION: n = A,T,C or US-09-918-995-1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 44516
                                                                                                                                                                                                                                        Sequence 74582, Application US/10437963 Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44516, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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Matches
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Best Local 9
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         APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa Thomas APPLICANT: Kovalic David
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APPLICANT: Cao Yongwe
CURRENT APPLICATION NUMBER: US/10/437,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: PAT_MRT3847_140197C.1
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NAME/KEY: misc_feature
LOCATION: (1)...(473)
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Kovalic David K
                                                                                                        Boukharov, Andrey A.
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100.0%; Pred. No.
tive 0; Mismatc
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Pred. No. 4e+02;
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. 3.1e+02;
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RESULT 10
US-10-027-632-215235
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; ORGANISM: Human
US-10-027-632-215234
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US-10-027-632-215234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29
Sequence 215235, Application US/10027632
publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 215334
LENGTH: 599
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Best Local
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SEQ ID NO 74582
LENGTH: 558
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocal Similarity
                                                                                                                                                                                                                                                                                                  206 TCTAGAGACGGTCTGGCT
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Pred. No. 3.
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Pred. No. 3.9e+02
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APPLICATION NUMBER: US 60/198,676

2000-07-12 NUMBER: US 2000-04-20

FILING DATE: APPLICATION N FILING DATE:

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US-10-027-632-215234
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; ORGANISM: Human
US-10-027-632-215235
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                   ; ORGANISM: Human
US-10-027-632-215234
                                                                                                                                                                                                           SEQ ID NO 215234
LENGTH: 599
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Publication No. US20030204075A9
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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CURRENT FILING DATE: 2002-04-30
CRICK APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/198,676
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                                                                                                                                                                                           TYPE: DNA
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les 16; Conserv
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 TCTAGAGACGGTCTGGCT 223
                                     TCTAGTGACGGTCTCGCT 18
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Pred. No. 3.9e
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Pred. No. 3
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US-10-027-632-215235
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Publication No. US20040172684A1
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SEQ ID NO 215235
LENGTH: 599
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LENGTH: 675
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Best Local Similarity
                                                                                                                 Query Match
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CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
FILE REFERENCE: 38-21(53535)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-02-24
PRIOR ALPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                 ORGANISM: Sorghum bicolor FEATURE:
                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                Local
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361
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TCTGGTGACGGTCTCACT 378
                                     TCTAGTGACGGTCTCGCT 18
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Pred. No. 3.9e+02;
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Pred. No. 3
                                                                               Mismatches
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RESULT 12

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; Sequence 5769, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 5769
; LENGTH: 28573
; TYPE: DNA
; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 82321
LENGTH: 3461
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
COTHER INFORMATION: Clone ID: PAT_MRT4530_81762C.1
US-10-437-963-82321
Search completed: October 1, 2004, 08:53:45 Job time: 75.304 secs
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US-10-741-601-5769
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Best Local Similarity 88.9%;
Matches 16; Conservative
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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Local Similarity 88.9%;
es 16; Conservative
                                                                                  27720 TCTGGAGACGGTCTCGCT 27737
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Barbazuk, Brad
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Pred. No. 3.6e+02;
0; Mismatches 2;
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Pred. No. 3.8e+02;
0; Mismatches 2;
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Gapop 10.0 , Gapext 1.0
   27513289 seqs, 14931090276 residues
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Maximum Match 100%
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gb htc:*
gb est4:*
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UI-D-GC1-aag-p-10-0-UI.sl UI-D-GC1 Alexandrium tamarense cDNA clone
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CF947869.1 GI:38452687
KEYMORDS
SOURCE
Alexandrium tamarense
ORGANISM
ALEXANDRIUM
Lemandrium
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Result No.

Score

Query Match

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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621 855 870 936

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CF947869 CG856355 CG856546 CNS03M43

CF947869 UI-D-GC1-CG856355 ZMMBBC026 CG856546 ZMMBBC026 AL250284 Tetraodon

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Zea mays subsp. mays
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Burmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 855)
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.
Sequencing of the maize genome at PGIR (2003c)
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                    Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
                                                                                                                                                              Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                       Unpublished (2003)
Contact: Bharti, A.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG856355.1 GI:38429068
                                                                                                          190 Frelinghuysen Road, Piscataway,
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primer: SP6
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/strain="CCMP 1598"
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LIB=UI-D-GC1
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High quality sequence start: 527
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                        Tel: 732 445 3801
Fax: 732 445 5735
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Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                             Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2003)
                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                        Email: bharti@waksman.rutgers.edu
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                                                                                                                                                       /lab_host="E. coli DH10B"
/clone_lib="ZMMBBc (EcoRI)"
                                                                                                                                                                                    /db_xref="taxon:4578"
/clone="ZMMBBc0260N11"
                                                                                                                                                                                                                                   /organism="Zea mays subsp.
/mol_type="genomic DNA"
/cultivar="B73"
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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
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:lone_lib="ZMMBBc (EcoRI)"
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                     genomic survey sequence. CC623601 CC623601.1 GI:31990367
                                                                                          OGVAZ30TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0493E12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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Tetraodon nigroviridis genome survey sequence T7 end of clone
037103 of library G from Tetraodon nigroviridis, genomic survey
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/clone_lib="G"
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                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Tetraodon nigroviridis"
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Pred. No. 1.6e+03;
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                                                                                        Email: bharti@waksman.rutgers.
Seq primer: T7
Class: BAC ends
                                                                                                                                              Tel: 732 445 3801
Fax: 732 445 5735
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CG416849.1 GI:34561694
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Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                   University
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                                                                                                                                                                                190 Frelinghuysen Road,
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                                                                     quality sequence
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/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
                                                        Location/Qualifiers
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/strain="B73"
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ORGANISM
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Zea mays subsp. mays (maize)

Zea mays subsp. mays

Zea mays subsp. mays

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

clade; Panicoideae; Andropogoneae; Zea.
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1 (bases 1 to 714)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Unpublished (2002)
Other GSSs: OGVAZ30TV
                                               Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                         Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c) Unpublished (2003)
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ZMMBBC0026J18f ZMMBBC (EcoRI) Zea mays subsp. mays genomic clone
ZMMBBC0026J18 5', genomic survey sequence.
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/note="Vector: pBCSK: DITE DNA library"
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100.0%; Pred. No. 2.4e+03;
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BZ819718 955 bp DNA linear GSS 18-M
PUGCC66TD ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTa334L11,
genomic survey sequence.
BZ819718
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(bases 1 to 817)

Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGVAZ30TH
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Tel: 301-838-5843
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methylation filtered genomic DNA library"
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/strain="B73"
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/db_xref="taxon:4578"
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                                                                                                                                                                    Maize Genomics Consortium Unpublished (2003) Other GSSs: PUGCC66TD
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          Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                      clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 986)
Whitelaw, C.A., Quackenbush, J., Van Aken
                                                                                                                                                                                                                                                                                                                                          Zea mays
                                                                                                                                                                                                                                                                                                                                                                              BZ819712.1
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                              genomic survey sequence.
BZ819712
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1 (bases 1 to 955)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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Class: sheared ends.
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BZ819718.1 GI:29034540 GSS.
                                                  Seq primer: TR
                                                                  Email: whitelaw@tigr.org
                                                                                   Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                     9712 Medical Center Drive,
                                                                                                                                                      Contact: Cathy Whitelaw
                                                                                                                                                                                                                        Bennetzen, J
                                                                                                                                                                                                                                        Resnick, A., Fraser, C.M.,
                                                                                                                                                                                                                                                                                                                                                                Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bennetzen, J
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/clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4-TOFO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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/strain="B73"
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tive 0;
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                                                                                                                     Rockville,
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Y., San Miguel,P., Ma,J. and
                                                                                                                     MD 20850, USA
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RESULT 11
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CA991730/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beijing AgroBiotechnology Research Center
Haidian District, Ban-Jing Rd., Beijing 100089, China
Tel: 86 10 5150 3980
Fax: 86 10 5150 3980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Chinese cabbage 
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rcmal@yahoo.com
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Rongcai, Ma
Plant Functional Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed sequence tags of heading leaf during the heading process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gao, R.J.,
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larity 100.0%;
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/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0
CoT selected genomic DNA library"
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                                                                                                                                                                                                                  /dev_stage="folding stage"
/lab host="E.coli DH10B(ZIP)"
/clone lib="GIBCOBRL CAT. NO. 19643-014"
/clone lib="GIBCOBRL CAT. NO. 19643-014"
/note="Vector: pZL1; Site 1: Not1; Site 2: Sal1; cDNA
/note="Vector: pZL1; Site 5: Not1; Site 6: Sal1; cDNA
library was constructed by SUPERSCRIPTTM Lambda System for
cDNA Synthesis and Cloning (GIBCOBRL,CAT.NO.19643-014)"
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     /sub_species="pekinensis"
/db_xref="taxon:51351"
/tissue_type="heading leaf"
                                                                                                                                                                                                                                                                                                                                                                         /organism="Brassica rapa subsp. pekinensis"
/mol_type="mRNA"
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Pred. No.
                                                                                                                                                   Score 15.4; DB 14;
Pred. No. 4.1e+03;
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855 California Ave, F
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 486)
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Plate: 1007106 column: 29
Class: transposon-tagged.
Location/Qualifiers
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Contact: Walbot V
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                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="1007 - RescueMu Grid H"
/clone lib="1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BgIII;
RescueMu is 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid H was grown at Berkeley in 2001. DNA
was extracted from leaf punches, double digested using
BamHI and BgIII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/cultivar="mixed background
/db_xref="taxon:4577"
/tissue_type="leaf"
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lab_host="DH10B"
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94.1%;
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SueMu Grid H Zea mays genomic, genomic
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Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
close per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/.cDNA
clones and filters are distributed via the Resource Center/Primary
                                                                                                                                                                                                                                                                                                                                                Poustka, A.J., Groth, D., Hennig, S., Thamm, S., Cameron, A., Bec Reinhardt, R., Herwig, R., Panopoulou, G. and Lehrach, H.
Generation, annotation, evolutionary analysis, and database integration of 20,000 unique sea urchin EST clusters Genome Res. 13 (12), 2736-2746 (2003)

Contact: Poustka AJ
Laboraty 145, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innestr. 63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1138
Tea: +49 30 8413 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD31726.

StrPu621.001629 Sea urchin unfertilised egg cDNA library MPMGp621 Strongylocentrotus purpuratus cDNA clone
Strongylocentrotus purpuratus cDNA clone
MPMGp621G2116;MPI_621_16G21 5', mRNA sequence.
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Tissue Procurement: DCTD/DTP/Gazdar
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="MARGE:3876716"
/tissue_type="large cell carcinoma"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="MIH_MCC_68"
/clone_tib="NIH_MCC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
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Pred. No. 4.2e+03;
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Matches 16; Conserv
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BJ130132.1
EST.
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BJ130132
                                                                                                                                                                                                                                                                                                                                                                                                                                               A complementary view of the C.elegans genome Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                    Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
Caenorhabditis elegans
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BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGAATGTG 3' (M13FSP)
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
                                                                                                                                                                                                                                                                                                            Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BJ130132 mpublished oligo-capped cDNA library, C. elegans L1
BJ130132 unpublished oligo-capped cDNA library, C. elegans L1
Caeporhabditis elegans cDNA clone yk1039d08 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Sugano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                      Fax: 81-559-81-6855
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    Conservative
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/dev_stage="embryonic Ohr"
/lab_host="E.coli, XL1 blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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/clone="MPMGp62162116;MPI_621_16G21"
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/mol_type="mRNA"
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                                                                                                                  clone_
                                                                                                                                                    tissue_type="whole animal"
                                                                                                                                                                                                                                                                        organism="Caenorhabditis elegans"
                    88.9%;
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                                                                                              _stage="L1"
ne_lib="unpublished oligo-capped
ns_L1 stage"
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Pred. No. 4.5e+03;
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                                      DB 12;
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LOCUS
Search completed: October 1, 2004, 08:01:43 Job time : 259.333 secs
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                      456 TCNAGTGACGGGCTCGCT 473
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                                                                                            1 TCTAGTGACGGTCTCGCT 18
                                                                                                                                            ch 85.6%; Score 15.4; DB 12; Length 629; l Similarity 88.9%; Pred. No. 4.5e+03; 16; Conservative 0; Mismatches 2; Indels 0
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Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 629)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           629 bp mRNA linear EST 24-JAN-2002
BJ147480 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone ykl251f07 3', mRNA sequence.
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/dlone="ykl251f07"
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/dev stage="L1"
/clone_lib="unpublished oligo-capped cDNA library, C.elegans L1 stage"
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RESULT 1 AAV83706 ID AAV8 XX AAV83706 standard; DNA; 18 ВP

AAV83706; Species-specific probe targeted to the internal transcribed spacer 2. 26-FEB-1999 (first entry)

Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus; M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus; R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunniphamella elegans; Pseudallesheria bydii; Scedosporium apiospermum; Penicillium notatum; Sporothrix schenkii; filamentous fungus; ss.

Synthetic. WO9850584-A2 modified_base Location/Qualifiers /*tag= a /note= "labelled with digoxigenin"

01-MAY-1998; 12-NOV-1998. 02-MAY-1997; 97US-0045400P. 98WO-US008926

Morrison <u>ج</u> Reiss E, Aidorevich L, Choi JS;

(USSH) US DEPT HEALTH & HUMAN SERVICES.

WPI; 1999-034737/03.

New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothrix species

Claim 47; Page 23; 45pp; English

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RESULT 2
AAV70851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus; M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus; R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum; penicillium notatum; Sporothrix schenkii; filamentous fungus; ss.
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26-FEB-1999
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                                                                  The present sequence represents an internal transcribed space and adjacent regions. Probes can be derived from the present which are species-specific. The specification also describes which are species specific and a species selected from the present of the specification and the species selected from the probes for identifying a species selected from the species of the species o
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                           Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. n. Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus,
                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                      New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudoallescheria boydii, Penicillium and Sporothr
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Fusarium solani,

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Matches 18
                                                    The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans, A. spergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans, A. indicus, M. circinilloides f. circinelloides, R. Rizopus oryzae, R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallesheria boydii (telecmorph of Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenkii. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus; R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid probes for f
Aspergillus, Fusarium, Mucor,
Cunninghamella, Pseudoallesch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Internal transcribed
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 12; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morrison CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           terreus; A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-034737/03.
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18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcribed spacer 2; ITS2; probe; Aspergillus flavus; us; A. nidulans; Fusarium solani; F. moniliforme; Mucorosus; M. plumbeus; M. indicus; A. fumigatus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sporothrix schenkii; filamentous fungus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spacer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for filamentous fungi - for detecting e.g.
Mucor, Rhizopus, Rhizomucor, Absidia,
llescheria boydii, Penicillium and Sporothr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aidorevich L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (ITS2) and adjacent regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
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Pred. No.
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                                                                                                 The invention relates to novel steroid compounds derived from the African CC soil fungus Fusarium sp. WF6381 (ATCC 74469) which act as inhibitors of CC HIV integrase. The invention encompasses cultures of Fusarium sp. MF6381.

CC The invention also relates to a composition comprising a compound of the invention in combination with an AIDS antiviral agent, an immunomodulator and an antiinfective agent. The compounds of the invention may be used in the inhibition of HIV integrase and in the prevention and treatment of CC the inhibition of HIV integrase and in the prevention may be treated: CC AIDS (acquired immunodeficiency syndrome); ARC (AIDS related complex); CC both symptomatic and asymptomatic HIV infection; and actual or potential CC exposure to HIV. The compounds may be used to isolate HIV integrase mutants which are potentially useful as screening tools for antiviral CC competitive inhibition). The present sequence represents the ribosomal DNA (rDNA) internal transcribed spacer (ITS) region of Fusarium sp.

CC MF6381, which may be used to characterise MF6381. (Updated on 15-SEP-2003
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Best Local S
Matches 18
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Matches 18; Conserv
                                                             Sequence 502
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                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                               New steroid compounds are HIV integrase inhibitors used for treating infection and AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Singh SB, Zink DL,
Dombrowski AW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MERI ) MERCK & CO INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    symptomatic infectior combination therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469 HIV integrase inhibitor; steroid compound; human immunodeficency virus; acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex; symptomatic infection; asymptomatic infection; potential HIV exposure;
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14-NOV-2000
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                                                                                           standardise
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100.0%; Score 18; DB ilarity 100.0%; Pred. No. 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Page 14; 113pp; English.
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                                                             ВP;
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                                                                                           be used field)
                                                           A; 144 C; 118 G; 113
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Pred. No. 15;
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Gaps
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RESULT 6
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AAV62592 standard; DNA; 503

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RESULT 5
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Best Local Similarity
                                                                                                                                                                         A novel method for the detection of plant pathogenic strains of fungies. Septoria nodorum, S.tritici, Pseudocercosporella herpotrichoides, Mycosphaerella fijiensis, M.musicola or Fusarium spp, involves the PCR amplification of sequences found in the internal transcribed region (ITS) of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93 and AAT05357-72. These primers are derived from the ITS sequences of these fungi (AAT05394-T05404 and AAQ94398) and are strain specific. The amplification products of the reactions using these primers can be used with the capture primers AAT05378-93 in colourimetric assays. The primers and ITS DNAs can be used for the detection of specific fungal pathogen
                                                                                                                   Sequence 503 BP; 131 A; 127 C; 108 G; 116 T; 0 U; 21 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-383005/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ligon JM, Beck JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gibberella zeae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudocercosporella herpotrichoides; Mycosphaerella fijiensis; PCR; Mycosphaerella musicola; amplification; primer; ribosomal RNA gene; internal transcribed region; strain; capture; colourimetric assay; isolate; development; population; random amplified polymorphic DNA; ss.
                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 55; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 plant fungal pathogens
                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding intervening transcribed sequence - used for detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9529260-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusarium graminearum internal transcribed spacer sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-APR-1995;
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CCCAACTTCTGAATGTTG 468
                            CCCAACTTCTGAATGTTG 18
                                                                                                                                                 and in monitoring disease development i on 16-OCT-2003 to standardise OS field)
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                                                          Conservative
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(first entry)
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Pred. No.
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Fusarium graminearum PCR amplified ITS region consensus DNA sequence

17-OCT-2003 17-DEC-1998

(revised) (first entry)

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451 CCCAACTTCTGAATGTTG 468

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                                                                                                       This represents the consensus DNA sequence of the internal transcribed spacer (ITS) region that was PCR amplified from Pusarium graminearum isolates, R-8417, R-8422 and R-8546. The invention provides a DNA molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal pathogen, where the DNA molecule consists of an ITS sequence selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium conniliforme, Septoria avenae or Microdochicum nivale. A method for detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F. cavenaceum and M. nivale isolates is also provided. The method comprises isolating DNA from a plant leaf infected with at least one of the above pathogens and amplifying parts of the ITS sequence of the pathogen(s) C pathogens and amplifying parts of the ITS sequences. The pathogen(s) are detected by visualising the amplified part of the ITS sequence.

(*C (Updated on 17-OCT-2003 to standardise OS field)
                              Matches
                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen; Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant; Septoria avenae; Microdochicum nivale; Fusarium poae; Fusarium avenaceum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR; nucleic acid detection; ss.
                                                                                Sequence 503 BP; 131
                                                                                                                                                                                                                                                                                                                    Claim 2;
                                                                                                                                                                                                                                                                                                                                                              DNA isolated from fungal RNA,
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-541745/46
                                                                                                                                                                                                                                                                                                                                                                                                                    Beck
                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVS ) NOVARTIS FINANCE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-APR-1995;
15-OCT-1996;
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                                         Local
                           Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                    Fig 3; 56pp;

    used for detecting

 CCCAACTTCTGAATGTTG 18
                           100.0%; Score 18; DB llarity 100.0%; Pred. No. 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US004712.
96US-00722187.
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/note= "5.8S rRNA
313..466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156. .312
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/note= "3'
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/note= "ITS 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "ITS 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "5'
                                                                                A; 127 C;
                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end of small subunit rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end of large subunit rRNA gene"
                                                                                                                                                                                                                                                                                                                                               and its internal transcribed space fungal pathogens in plant tissue.
                                                                                 108 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene'
                                                                                   116 T; 0 U;
                                                       В
                                                       2
                              0;
                                                                                                                                                                                                                                                                                                                                                               transcribed spacer
                                                      Length 503;
                                                                                    21 Other;
                               Indels
                              0
                              Gaps
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RESULT 8
AAT05400
ID AATC

AAT05400 standard; DNA; 504

ВP

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                                               Matches
                                                                      Query Match
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25-MAR-2003
06-JAN-1999
                                                                                                                This sequence represents an internal transcribed spacer (ITS) sequence of the invention. The primer pairs, based on the ITS sequences, are used for the PCR amplification detection of wheat Microdochium and Fusarium fungal pathogens, especially M. nivale, F. graminearum, F. culmorum, F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different strains of fungi show different symptoms during infection, which may or may not be due to infection. Early identification of the strain causing the infection allows early, and more specific fungicidal treatment. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV59029
                                                                                                                                                                                                                                                                                                                                                   Beck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gibberella zeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F. graminearum internal transcribed spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV59029;
                                                                                                                                                                                                                                                                           Wheat pathogen internal transcribed spacer sequences - used as a basis for primers for the species-specific polymerase chain reaction detection of the pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                              Sequence
                                                                                                                                                                                                                                                      Disclosure; Col 23-24; 20pp;
                                                                                                                                                                                                                                                                                                                           WPI; 1998-593995/50
                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen; fungal pathogen identification; infection identification; ss.
                                                                                                                                                                                                                                                                                                                                                                          (NOVS ) NOVARTIS FINANCE CORP
                                                            Local
 451
                                              18;
                       سر
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 503
                                                                                              503
                       CCCAACTTCTGAATGTTG 18
  CCCAACTTCTGAATGTTG
                                               Conservative
                                                                                              BP; 131 A; 127 C; 108 G; 116 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
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/note= "ITS1"
313. .466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
/note= "ITS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                          100.0%;
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  468
                                               0
                                                                                                                                                                                                                                                      English.
                                                            Score 18;
Pred. No.
                                                Mismatches
                                                             16;
                                                                        DB
                                                                        <u>ب</u>
                                                  0
                                                                       Length 503;
                                                                                                 21 Other;
                                                  Indels
                                                  0,
                                                  Gaps
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RRESULT 9
AAV6250
ID AAVE
XX AAVE
XX AAVE
XX AAVE
XX Inte
KW Fuse
KW Fuse
KW Sept
KW Sept
KW Sept
KW Sept
XX XX YESE
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            A novel method for the detection of plant pathogenic strains of fungi e.g. Septoria nodorum, S.tritici, Pseudocercosporella herpotrichoides, Mycosphaerella fijlensis, M.musicola or Fusarium spp, involves the PCR amplification of sequences found in the internal transcribed region (ITS) of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93 and AAT05357-72. These primers are derived from the ITS sequences of these fungi (AAT05394-T05404 and AAQ94398) and are strain specific. The amplification products of the reactions using these primers can be used with the capture primers AAT05378-93 in colourimetric assays. The primers and ITS DNAs can be used for the detection of specific fungal pathogen isolates and in monitoring disease development in plant populations
                               Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen; Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant; Septoria avenae; Microdochicum nivale; Fusarium poae; Fusarium avenaceu PCR; nucleic acid detection: 68.
                                                                                                              Fusarium culmorum
                                                                                                                                              17-DEC-1998
                                                                                                                                                                              AAV62591;
                                                                                                                                                                                                           AAV62591 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding intervening transcribed sequence - plant fungal pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-383005/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusarium culmorum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Bseudocercosporella herpotrichoides; Mycosphaerella fijiensi Mycosphaerella musicola; amplification; primer; ribosomal RN internal transcribed region; strain; capture; colourimetric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusarium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                             457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Page 54-55; 65pp; English.
                                                                                                                                                                                                                                                                                                                      ۲
                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                           CCCAACTTCTGAATGTTG
                                                                                                                                                                                                                                                                                                                          CCCAACTTCTGAATGTTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           culmorum internal transcribed spacer sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           development; population; random
                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 18; DB 2; llarity 100.0%; Pred. No. 16; Conservative 0; Mismatches
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-00233608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US004712.
                                                                                                             PCR amplified ITS region consensus DNA sequence
                                                                                                                                                                                                                                                                                           474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain; capture; colourimetric assay; sion; random amplified polymorphic DNA; ss
                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                      Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used
                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection
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                                                                                                                                                                                                                                                                                                                                                        0
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                                                plant;
avenaceum;
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of.
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Fusarium culmorum

culmorum

internal transcribed spacer.

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RESULT 10
AAV59028
ID AAV59
XX
AC AAV59
XX
AC AAV59
XX
DT 25-MA
DT 06-JA
XX
DE F. CU
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                                                                                                                                                                        S
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                      This represents the consensus DNA sequence of the internal transcribed spacer (ITS) region that was PCR amplified from Fusarium culmorum isolates, R-5106, R-5126 and R-5146. The invention provides a DNA molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal pathogen, where the DNA molecule consists of an ITS sequence selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium moniliforme, Septoria avenae or Microdochicum nivale. A method for detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F. avenaceum and M. nivale isolates is also provided. The method comprises isolating DNA from a plant leaf infected with at least one of the above pathogens and amplifying parts of the ITS sequence of the pathogen(s) by PCR using specific primers from within these sequences. The pathogen(s) are detected by visualising the amplified part of the ITS sequence
                                                            AAV59028;
                       06-JAN-1999
                                    25-MAR-2003
                                                                                                                                                                                                                                                    Sequence 504 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA isolated from fungal RNA, sequence - used for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                     AAV59028
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 3; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-541745/46.
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15-OCT-1996;
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                                                                                                                                                                  CCCAACTTCTGAATGTTG 18
                                                                                     standard;
                                                                                                                                                   CCCAACTTCTGAATGTTG 474
                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative 0
                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-US004712.
96US-00722187.
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/note= "5.8S
319. .472
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/note= "ITS
473. .504
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/note= "3'
13 .161
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/note= "5'
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/note= "ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                    DNA; 504
                                                                                                                                                                                                                                                  A; 132 C; 113 G; 122 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 end
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                                                                                      ВP
                                                                                                                                                                                                  0
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                                                                                                                                                                                                              Score 18; DB
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and its internal transcribed spacer fungal pathogens in plant tissue.
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Fi
                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                small subunit rRNA gene"
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                                                                                                                                                                                                                         2;
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;:
                                                                                                                                                                                                                                                  U; 4 Other;
                                                                                                                                                                                                                         Length 504;
                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                   Gaps
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RESULT 11
AASO8426
ID AASO8
XX ASO8
XX ASO8
XX Inter
XX Inter
XX Inter
XX Inter
XX Sharr
XX Sharr
XX WO200
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wheat pathogen internal transcribed spacer sequences - used as a basis for primers for the species-specific polymerase chain reaction detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fungal
                                    Fusarium culmorum
                                                            Internal transcribed Sharp eyespot; fungal
                                                                                                                           26-SEP-2001
                                                                                                                                                                                                                                                                                                                                       Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 21-22; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-593995/50
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             WO200151653-A1
                                                                                                  Internal transcribed spacer,
                                                                                                                                                                             AAS08426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the pathogens.
                                                                                                                                                                                                                                           457
                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al transcribed spacer; ITS; Microdochium; Pusarium; wheat pathogen identification; infection identification; ss.
                                                                                                                                                                                                                                                                   Н
                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                    PR field.)
                                                                                                                                                                             standard; DNA;
                                                                                                                                                                                                                                                        CCCAACTTCTGAATGTTG
                                                                                                                                                                                                                                           CCCAACTTCTGAATGTTG 474
                                                                                                                                                                                                                                                                                         100.0%; Silarity 100.0%; IConservative 0;
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-00905314.
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/note= "ITS1"
319. .472
                                                             fungal
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/note= "ITS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 161
                                                                          spacer; ITS;
                                                             pathotype
                                                                                                                                                                             504
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                                                                                                                                                                             ВÞ
                                                                                                                                                                                                                                                                 18
                                                                                                  ITS,
                                                                                                                                                                                                                                                                                                        Score 18; DB
Pred. No. 16;
                                                                                                                                                                                                                                                                                            Mismatches
                                                             identification; isolate 62215
                                                                          fungal pathogen; ss; wheat disease;
                                                                                                 region #16.
                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                            U; 4 Other;
                                                                                                                                                                                                                                                                                                                   Length 504;
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RESULT 12
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Curmorum, isolate 62215. The ITS DNA sequences are useful for detecting Rhizoctonia cerealis, a fungal pathogen of wheat causing Sharp eyespot, for monitoring disease development in plant population, and for providing detailed information on the development and spread of specific pathogen races over extended geographical areas. The DNA sequences are specifically used as primers in PCR-based analysis for the identification of fungal pathotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2000;
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                                                                   Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 31; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New internal transcribed spacer DNA sequences, useful for identifying fungal pathogen, particularly Rhizoctonia cerealis, and for monitoring disease development in plant population.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-442154/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibberella zeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondria; fungal pathogen; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Internal transcribed spacer RNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is an internal transcribed spacer (ITS) region from Eusarive transcribed spacer (ITS) region from Eus
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                                                                                                                                                                                                         WPI; 2003-363229/34.
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Pred. No. 16;
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Claim 5;

Page 38; 44pp; English

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RESULT 14
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Matches 18
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Best Local (
                                                                                                                                                                                       This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods are primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present sequence represents an internal transcribed spacer RNA encoding sequence
                                                                                                                                                                                                                                                                                         Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
          ACC50002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods and primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present sequence represents an internal transcribed spacer RNA encoding sequence
                                                                                                                                                                     Sequence 522
                                                                                                                                                                                                                                                                  Claim 5; Page 38; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusarium subglutinans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondria; fungal pathogen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Internal transcribed
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          standard;
                                                                                           CCCAACTTCTGAATGTTG
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           DNA;
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                                                                                                                                                                    G; 124 T;
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                                                                                                                                          Length 522;
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RESULT 15
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(Updated
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                                                                                                                                                                            14-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
                  24-SEP-2001; 2001US-00961755.
                                                                03-APR-2003
                                                                                                                                Mitochondria; fungal
                                                                                                                                                   Internal transcribed spacer RNA encoding
                                                                                                                                                                                                                       ACC50001
                                         19-SEP-2002; 2002WO-US030311
                                                                                      WO2003027635-A2
                                                                                                                                                                                                                                                                                                                                                                     Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beck JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-SEP-2001; 2001US-00961755
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                                                                                                                                                                                                                                                                                            CCCAACTTCTGAATGTTG 18
                                                                                                                                                                                                                        standard;
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(first entry)
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                                                                                                                                                                                                                        DNA;
                                                                                                                                pathogen; ds
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(SYGN) SYNGENTA PARTICIPATIONS

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                                                                                                                                                  Query Match 100.0%; Score 18; DB 7; Length 534; Best Local Similarity 100.0%; Pred. No. 16; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                 This invention relates to the detection of a fungal pathogen comprising isolating DNA from a plant leaf infected with a pathogen. The methods and primers are useful for identifying fungal isolates of fungal pathogens and monitoring of disease development in plant populations. The present sequence represents an internal transcribed spacer RNA encoding sequence
                                                                                                                                                                                                                               Sequence 534 BP; 135 A; 149 C; 130 G; 120 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a fungal pathogen, useful for monitoring disease development, comprises subjecting the DNA to PCR amplification using at least one primer having sequence identity with at least 10 contiguous nucleotides of Fusarium spp.
                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 38-39; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-363229/34.
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Database Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Maximum Minimum Title: Perfect score: OM nucleic -Total number Searched: Scoring table: Sequence: 92: DB 80 seq Seq of hits satisfying chosen parameters: nucleic search, using length: IDENTITY_NUC US-10-046-955-59 18 3470272 seqs, Gapop 10.0 , October GenEmbl: * cccaacttctgaatgttg gb pat:
gb ph:
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Million cell updates/sec REFERENCE AUTHORS RESULT 1 AR206453 LOCUS Result a a TITLE ö

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE ORGANISM DEFINITION ACCESSION VERSION KEYWORDS JOURNAL Score Unknown. Unknown. Sequence AR206453 1 (bases 1 to 18) Morrison, C.J., Reiss, B., Aidorevich, L. and Choi, J.Soo. Nucleic acids for detecting Aspergillus species and ot filamentous fungi Patent: US 6372430-A 59 16-APR-2002; AR206453.1 GI:21505059 Unclassified. Match 59 Length from patent В HR206453 HR206401 HR206401 HR206400 HR206400 HR206400 HR206400 HR206400 HR206400 HR206400 HR206400 HR206400 HR2062902 ARF162899 ARF162899 ARF162899 ARF162899 ARF162899 ARF162893 ARF16333 ARF16333 ARF10333 ARF11033 ARF162893 ARF11033 SD ALIGNMENTS 18 bp I S 6372430. DNA linear AF162900 AF339418 AY074751 AF117921 AF162901 AF162902 AF162898 AF162899 AF117922 AR206400 BD083591 AF165875 AF502862 AY160207 AY160209 AF161222 AY210325 AY143084 AF502788 AF162897 AF162903 AF111 AY210331 Description other PAT 20-JUN-2002 Unculture Ascomycet Pusarium Fusarium Leaf litt Fusarium Sequence Nucleic a Nucleic a Nectria l Nectria s Fusarium Nectriah Unculture Fungal is Fusarium Leaf litt Fusarium Leaf litt Fusarium Fusarium Fusarium Fusarium Fusarium Fusarium Theobroma Theobroma Theobroma Theobroma Fusarium Fusarium Fusarium Fusarium Nucleic Nectria Gibberell Sequence

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PD 11-DEC-2001
PR 02-MAY-1998 JP 1998548275
PR 02-MAY-1997 US 66/045400
PI CHOI
PI CHOI
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Strandedness: Single;
CC Topology: Linear;
FH Key Lication/Qualifiers.
                                         AY226096 298 bp DNA Nectria haematococca 5.8S ribosomal RNA internal transcribed spacer 2, complete RNA gene, partial sequence.

AY226096
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Rhizopus microsporus
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 Nectria haematococca
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JP 2001525665-A/59.
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                                                                                                                                                                                                                                                                                                      /organism="Rhizopus microsporus"
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gene, partial sequence;
sequence; and 28S ribosomal
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BD083592.1 GI:22629202
BD083592.1 GI:22629202
JP 2001525665-A/7.
Gibberella fujkuroi
Gibberella fujkuroi
Gibberella fujkuroi
Finkaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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Sequence 7
AR206401
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordari
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
1 (bases 1 to 298)
Millar, B.C., Xu, J. and Moore, J.E.
Direct Submission
                                                                                                                       Nucleic acids for detecting filamentous fungi.
                                                                                                                                                                                                                                                                                                                                                                         filamentous fungi
Patent: US 6372430-A 7 16-APR-2002;
Location/Qualifiers
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Morrison, C.J., Reiss, E., Aldorevich, L. a
Nucleic acids for detecting Aspergillus
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/mol_type="unassigned
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L Patent: JP 2001525665-A 7 11-DEC-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O
CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND
PREVENTION TECHNOLOGY TRANSFER OFFICE
OS FUBBRIUM MODALLIFORME
PN JP 2001525665-A/7
PD 11-DEC-2001
PF 01-MAY-1998 JP 1998548275
PR 02-MAY-1998 JP 1998548275
PR 02-MAY-1997 US 60/045400
PI CHRISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO
PI CHRISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO
PI CHRISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO
PI CHRISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO
PI CHOI
PC CIQQI/68
CC Topology: Linear;
Location/Qualifiers.
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AF117922
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1 (bases 1 to 310)

Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.

Nucleic acids for detecting Aspergillus species and other
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Nectriaceae; (
                                                                                                                                                                                                                                                                                                                                                                                                                       Gibberella fujikuroi
                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                            Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
                                                                                                                                                                                                                                                                               DNA probes
                                                                                                                                                                                                                                                                                                 Rapid differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF117922.1 GI:8570108
                                                                                                                                                                                                                                                                                                                                                    fujikuroi complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                  (bases 1 to 310)
oi,J.S., Westerman,J.M. and Morrison,C.J.
aifferentiation of filamentous fungi using species-specific
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                                                                                                                                                                                                                             J.S., Westerman, J.M. and Morrison, C.J.
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larity 100.0%;
Conservative 0
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   /product="5.8S ribosomal RNA"
159. .272
                                                                                                                                                                                             (09-SEP-1998) DBMD,
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/mol_type="genomic DNA"
/db_xref="taxon:5127"
                                                  /db_xref="taxon:5127"
                                                                 /mol_type="genomic DNA"
/strain="ATCC 38519"
/db_xref="ATCC:38519"
                                                                                                                                                          Location/Qualifiers
                                                                                                                        organism="Gibberella fujikuroi"
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Pred. No. 44;
D; Mismatches
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Gibberella; Gibberella
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VERSION
KEYWORDS
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AUTHORS
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Best Local
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Filamentous fungi

Detent: JP 2001525665-A 6 11-DEC-2001;

Patent: JP 2001525665-A 6 11-DEC-2001;

THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE

OS FUSSITION TECHNOLOGY TRANSFER OFFICE

OS FUSSITION 501801

PN JP 2001525665-A/6

PD 11-DEC-2001

PR 02-MAY-1998 JP 1998548275

PR 02-MAY-1997 US 60/045400

PI CHRISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO
                                                                                                                                                                                                                                                                                                  BD083591
BD083591.1 GI:22629201
JP 2001525665-A/6.
Fusarium solani
Fusarium solani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 CCCAACTTCTGAATGTTG 284
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Sequence
AR206400
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                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 319)

Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.

Nucleic acids for detecting Aspergillus species and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                filamentous fungi
Patent: US 6372430-A 6 16-APR-2002;
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Morrison, C.J., Reiss, E., Aidorevich, L. a
Nucleic acids for detecting Aspergillus
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 01-MAY-1998 JP 1998548275
02-MAY-1997 US 60/045400
CHRISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO
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/mol_type="unassigned DNA"
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Pred. No.
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other
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TITLE
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AUTHORS
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AF162901
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SOURCE
ORGANISM
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  AF162901
Fusarium
internal
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

1 (bases 1 to 319)
Choi,J.S., Westerman,J.M. and Morrison,C.J.
Rapid differentiation of filamentous fungi using species-speci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF117921 319 bp DNA
Nectria haematococca 5.8S ribosomal RNA
internal transcribed spacer 2, complete
RNA gene, partial sequence.
AF117921
AF117921.1 GI:8570107
                                                                                                                             Н
                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-SEP-1998) DBMD, 30333, USA
                                                                                                                                                                                                                                                                                                                                                                                                                        Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C
2 (bases 1 to 319)
Choi.J.S., Westerman, J.M. and Morrison, C.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCCAACTTCTGAATGTTG 18
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Similarity 100.0%; Pred. No.
18; Conservative 0; Mismatch
                                                                                                                                                                     Similarity
                                                                                                  CCCAACTTCTGAATGTTG
                                                                                                                             CCCAACTTCTGAATGTTG 18
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C12Q1/68
                                                                                                                                                          Conservative
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332 bp DNA linear equiseti 5.8S ribosomal RNA gene, partial transcribed spacer 2, complete sequence;
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/mol_type="genomic DNA"
/db_xref="taxon:169388"
                                                                                                                                                                                                                              /product="28S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:169388"
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                                                                                                                                                                                                                                                       'note="ITS2"
                                                                                                                                                                                                                                                                    product="internal transcribed
                                                                                                                                                                                                                                                                                                product="5.88 ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                     organism="Fusarium solani"
                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                    100.0%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                     . 272
                                                                                                  284
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lete sequence; and 28S ribosomal
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partial
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  l sequence;
and 28S ribosomal
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                              PLN 04-AUG-1999
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                           18;
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RNA gene, partial sequence.

AF162902 77.5000.
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Fusarium equiseti
Fusarium equiseti
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, mitosporic Hypocreales, Fusari
1 (bases 1 to 332)
                                                                                                                                                                                                                                                                  Submitted (28-JUN-1999) Biology, Spong, Chong Ro-Gu, Seoul 110-743, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       Fusarium pallidoroseum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-JUN-1999) Biology, Dong, Chong Ro-Gu, Seoul 110-743,
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AF162901
AF162901.1 GI:5690390
                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                            Similarity
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CCCAACTTCTGAATGTTG 18
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275. .>332
                                                                                                                  /product="internal transcribed 277. .>334
                                                                                                                                                                                        /db_xref="taxon:100904"
                                                                                                                                                                                                         /organism="Fusarium pallidoroseum"
/mol_type="genomic DNA"
/strain="MAFF 236666"
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/mol_type="genomic DNA"
/strain="MAFF 236724"
                                                                                                    /product="28S ribosomal RNA"
                                                                                                                                                             product="5.8S ribosomal RNA"
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29. .274
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                                           Score 18;
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3, Korea
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                                                                                                                                                               Fusarium oxysporum f. sp. fragariae
Fusarium oxysporum f. sp. fragariae
Fusarium oxysporum f. sp. fragariae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (Dases 1 to 335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCCAACTTCTGAATGTTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                      AF162899 335 bp DNA linear PLN 04-AUG-1999 FUSATIUM OXYSPORUM f. sp. fragariae 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence;
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                                                                                             Submitted (28-JUN-1999) Biology, SangMyung Dong, Chong Ro-Gu, Seoul 110-743, Korea
                                                                                                                                                                                                                                                                                                                      partial sequence; internal transcribed spacer and 28S ribosomal RNA gene, partial sequence. AF162899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-JUN-1999) Biology, SangMyung University, Dong, Chong Ro-Gu, Seoul 110-743, Korea Location/Qualifiers
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Fusarium oxysporum f. sp. conglutinans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
                                                                                                                                                 Min, B.R.
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1 (bases 1 to 335)
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                                                                    Chong Ro-Gu, Seoul 110-
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="internal transcribed 278. .>335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="5.8S ribosomal RNA"
l29. .277
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/mol_type="genomic DNA"
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note="forma_specialis: conglutinans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279
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AF162900
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Fusarium
Fusarium
                                                AP339418 338 bp DNA linear Fusarium oxysporum strain FS-1 5.8S ribosomal RNA sequence; internal transcribed spacer 2, complete ribosomal RNA gene, partial sequence.

AP339418
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                                       AF339418.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pusarium oxysporum f. sp. raphani
Fusarium oxysporum f. sp. raphani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
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AF162900.1 GI:5690389
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278. .>335
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forma specialis: fragariae"
<1. .128</pre>
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forma_specialis: raphani"
<1. .128</pre>
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129. .277
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                                                                                                                                                                                                                                                                                                                                      product="5.8S ribosomal RNA"
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                                       GI:24369714
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Pusarium oxysporum complex.

1 (bases 1 to 338)
Noley,P.W., Hatziloukas,E., Scott,D.L. Jr. and Carras,M.M.
Unpublished
Lupublished
1 (bases 1 to 338)
Noley,P.W., Hatziloukas,E., Scott,D.L. Jr. and Carras,M.M.
Lupublished
2 (bases 1 to 338)
Noley,P.W., Hatziloukas,E., Scott,D.L. Jr. and Carras,M.M.
Submitted (22-JAN-2001) Agricultural Research Service, U.S.
Department of Agriculture, 1301 Ditto Ave., Ft. Detrick, MD
21702-503, USA
100.0%; Score 18; DB 8; Length 338; ilarity 100.0%; Pred. No. 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                           /organism="Fusarium oxysporum"
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/strain="FS-1"
/db xref="taxon:5507"
/l...>338
                                                                                                                                                                         /note="contains 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
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1. .338
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Search completed: October 1, 2004, 05:17:04 Job time : 148.108 secs

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Result
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                                   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-08-905-314A-19
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US-08-905-314A-21
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US-08-905-314A-24
US-08-905-314-24
US-08-908-727-4
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Conservative

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Sequence 83, App...
Sequence 83, App...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2000-06-27 NUMBER OF SEQ ID NOS: 61
                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722
APPLICATION NUMBER: US 08/722
APPLICATION INFORMATION:
NAME: Meigs, U. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Beck,
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Detection of Fungal Pathogens Using the TITLE OF INVENTION: Polymerase Chain Reaction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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                                                                                                                                                                                                                                                      US 08/722,187
                                                                                                                                                  CGC 1739/PCT/CIP
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; NAME/KEY: misc_feature; LOCATION: 467..503; OTHER INFORMATION: /note= "5' end of large subunit; OTHER INFORMATION: rRNA gene"
US-08-887-480-83
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                   COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
            TELECOMMUNICATION INFORMATION: TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
                                                                               FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 1..9
OTHER INFORMATION: /note
OTHER INFORMATION: rRNA
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LOCATION:
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LOCATION: 10..155
OTHER INFORMATION: /note=
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                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                   CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
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LOCATION: 156..312
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                                                                                                                                                                         APPLICATION NUMBER:
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5827695
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                                                                                                                                                                                                                                                                                                                                      NO
                                                                                                                                                                                                                                                                                                                                                                      E: No. 5827695artis Corporation Patent Department
3054 Cornwallis Road
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ilarity 100.0%;
Conservative C
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313..466
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rRNA gene"
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Pred. No.
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SEQUENCE CHARACTERISTICS:

LENGTH:

nucleic acid

STRANDEDNESS:

single

TOPOLOGY:

linear

Andrea C.

1. The second se

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LOCATION: 467..503

COTHER INFORMATION: /note= "5'

OTHER INFORMATION: rRNA gene"

US-08-905-314A-20
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Patent No. 5955274
GENERAL INFORMATION:
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Best Local 9
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
FILING DATE:
        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
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ATTORNEY/AGENT INFORMATION:
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OTHER INFORMATION: /not
                                                                                                                                                                                                                                  COUNTRY:
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LOCATION: 156..312
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LOCATION: 313..466
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Local Similarity 100.0%; Pred. No. 2;
BS 18; Conservative 0; Mismatches
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                                                                                                                                                                                                               10532
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rRNA gene"
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                                                                                             US/08/722,187
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                                                                                                                                Version
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PCT-US95-04712-83; Sequence 83, Application PC/TUS9504712; GENERAL INFORMATION:
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Best Local (
                                                                                                                                 APPLICATION UNMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/233,608
FILING DATE: 04 APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION UNMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 91-541-8666
                                                                                            TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 919-541-860
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                         SEQUENCE CHARACTERISTICS:
LENGTH: 503 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBERS OF SEQUENCES: 86
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NAME/KEY: misc_feature

1..503
TOPOLOGY: 1
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LENGTH: 503 base pairs
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hawthorne STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Cloa-co-ive
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                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                        TELEPHONE:
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                                                                                                        919-541-8689
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Beck, James J
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DNA (genomic)
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internal transcribed spacer region of Fusarium graminearum
(fgram.con)"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                   Version #1.25
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Matches
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Patent No. 5814453
GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                              TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722
PILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION UNMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
INDIVIDUAL ISOLATE: (consensus sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
              NAME/KEY:
LOCATION:
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LOCATION:
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OTHER INFORMATION:
                                                                 NAME/KEY: misc feature LOCATION: 1..12
OTHER INFORMATION: /note OTHER INFORMATION: rRNA
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 OTHER INFORMATION:
                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                            LENGTH: 504 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                IOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                 CELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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1..503
                  misc_feature
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100.0%; Pred. No. 2;
tive 0; Mismatches
/note= "ITS 1"
                                                                 /note= "3' end of small subunit
rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "DNA sequence for the
internal transcribed spacer region of Fusarium graminearum
(fgram.con)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 08/722,187
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                                                                                                                                                                                            TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 18; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meige, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 473..504
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
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LOCATION: 1..12
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 473..504
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                                   NAME/KEY: misc_feature LOCATION: 1..12
                                                                                    ORGANISM: Fusarium culmorum INDIVIDUAL ISOLATE: R-5106, INDIVIDUAL ISOLATE: (consens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: No. 5827695artis Corporation Patent Department
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                               COPOLOGY:
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162..318
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319..472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DETECTION OF WHEAT FUNGAL PATHOGENS USING THE POLYMERASE CHAIN REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 18; D
100.0%; Pred. No. 2;
/note= "3' end of small subunit
rRNA gene"
                                                                                                       R-5106, R-5126, and R-5146
                                                                                    (consensus sequence)
                                                                                                                                                                                                                                                                          19:
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RESULT 10
US-08-722-187-82
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Best Local :
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APPLICANT: Ligon, James M
APPLICANT: Beck, James J
                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233
PILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC
                                                                                                                  TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
   FEATURE:
NAME/KEY:
                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: 1919-541-8666
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Detection of Fungal Pathogens Using TITLE OF INVENTION: Polymerase Chain Reaction NUMBER OF SEQUENCES: 86
                                   HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: NY
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LOCATION: 473.504
OTHER INFORMATION: /note= "5'
OTHER INFORMATION: rRNA gene"
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LOCATION: 162.318
OTHER INFORMATION: /note=
                                                                                    STRANDEDNESS:
                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10532
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OTHER INFORMATION:
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                                                                       TOPOLOGY:
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Similarity 100.0%; Pred. No.
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                                                                                                                    504 base pairs
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misc_feature
                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                    DNA (genomic)
                                                                                    single
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                                                                                                                                                                                                                                                                                                                 US 08/233,608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
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CURRENT APPLICATION NUMBER: US/09/481,293
; CURRENT FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 33
; SOPTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Fusarium culmorum
US-09-481-293-32
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COTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
US-08-722-187-82
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PCT-US95-04712-82
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US-09-481-293-32
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
EILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 82, Application PC/TUS9504712 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 18; Best Local Similarity 100.0%; Pred. No.
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Best Local Similarity
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APPLICANT: Barnett, Jason
TITLE OF INVENTION: PCR-Based Detection of Rhizoctonia cerealis
FILE REFERENCE: PB/5-31135P1
                                                                                                                                                                                                                                                                                                                APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                              ZIP: 10532
                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                               CITY: Hawthorne
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                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "DNA sequence internal transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (fculm.con)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spacer region of Fusarium culmorum
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REFERENCE/DOCKET NUMBER: CUTELECOMMUNICATION INFORMATION:

REGISTRATION NUMBER:

34,988

1739

TELEPHONE:

919-541-8689

919~541-8666

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Patent No. 5814453
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Best Local Similarity
                                                                                                                                                                            APPLICATION NUMBER: US/08/887,480
RILING DATE
CLASSIFICATION: 435
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/722,187
RILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Beck, James J
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INFORMATION FOR SEQ
                                                                                                     TELEFAX: 919-541-8687
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 52.
STREET: 52.
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Detection of Fungal Pathogens Using the TITLE OF INVENTION: Polymerase Chain Reaction
DRIGINAL SOURCE:
                 MOLECULE TYPE:
                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
OTHER INFORMATION:
                             STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1..504
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                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear LECULE TYPE: DNA
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                                                     : 545 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08887480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: No. 5814453artis Corporation 520 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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             DNA (genomic)
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internal transcribed spacer region of Fusarium culmorum
(fculm.con)"
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Pred. No.
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TELEFAX: (919) 541-8587
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 has a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/08905314A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Beck,
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NAME/KEY: misc_feature

**CATION: 336..488
                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                               ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Fusarium moniliforme INDIVIDUAL ISOLATE: 4551 IMMEDIATE SOURCE:
                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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LOCATION: 489..545
OTHER INFORMATION: /
OTHER INFORMATION: 1
                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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OTHER INFORMATION: /note=
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OTHER INFORMATION: /note=
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: No. 5827695artis Corporation Patent Department STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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31..178
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100.0%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             DETECTION OF WHEAT FUNGAL PATHOGENS USING THE POLYMERASE CHAIN REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "3'
rRNA gene"
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rRNA gene"
                                                                                                                                                                                                      US/08/905,314A
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                                                                                                           CGC 1944
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STRANDEDNESS: single

linear

DNA (genomic)

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RESULT 15
US-08-887-480-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 96, App....
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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OTHER INFORMATION: /not/
FEATURE:
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Beck, Ja
TITLE OF INVENTION:
TITLE OF INVENTION:
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 179.335
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NAME/KEY: misc
LOCATION: 1..30
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IMMEDIATE SOURCE:
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MOLECULE TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                STREET: 520 Whi
CITY: Tarrytown
STATE: NY
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LOCATION: 489.545
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
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OTHER INFORMATION:
                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                  ZIP: 10591
                                                                                                                                                                                                                                                                                                                                ADDRESSEE: No. 5814453artis Corporation STREET: 520 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
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LOCATION: 31..178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 100.0%; Score 18; DB: Local Similarity 100.0%; Pred. No. 2.1; es 18; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCCAACTTCTGAATGTTG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application
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rRNA gene"
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Search completed: October Job time: 7.93182 secs

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                                                                                                                  US-08-887-480-96
                                                        Matches
                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: 1.30
OTHER INFORMATION: /note=
OTHER INFORMATION: rRNA g
FEATURE:
NAME/KEY: misc feature
LOCATION: 31.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE:
CLONE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN: Fusarium poae INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus INDIVIDUAL ISOLATE: sequence)
IMMEDIATE SOURCE:
                                                                                                                                                                                     LOCATION: 338..48:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
STRAIN: Fusar
                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                            NAME/KEY: misc_feature
LOCATION: 490..546
OTHER INFORMATION: /note
OTHER INFORMATION: rRNA
                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 181..337
OTHER INFORMATION: /not
                                                                       Local
                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 338..489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 546 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
474
                   1 CCCAACTTCTGAATGTTG 18
                                                        18;
                                                                     h 100.0%; Score 18; DB 1;
Similarity 100.0%; Pred. No. 2.1;
CCCAACTTCTGAATGTTG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                 pCRFpoaeT427(1-2), pCRFpoaeT534(2-2), and pCRFpoaeT756(3-1)
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                        /note= "3'
rRNA gene"
                                                                                                                            /note= "5' end of large subunit
rRNA gene"
                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                   /note=
                                                      0;
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                                                                                                                                                                                                                                                         .8S rRNA gene"
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          end
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                                                                                                                                                                                                                                                                                                                                                                                          of small subunit
                                                        0;
                                                                                   Length 546;
                                                        Indels
                                                      0;
                                                      Gaps
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Mis Pose Blonk (USDIO)

Sequence 3660, A Sequence 11, App Sequence 19065, Sequence 11981,

e 3660, ... Appl

Sequence 57294, Sequence Sequence

120953, 270014, A 57294, A 94609, A

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications NA:*

1: /cgn2_6/ptcdata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptcdata/1/pubpna/US06_NEW_PUB.seq:*

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4: /cgn2_6/ptcdata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptcdata/1/pubpna/US06_PUBCOMB.seq:*

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13: /cgn2_6/ptcdata/1/pubpna/US09_NEW_PUB.seq:*

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18: /cgn2_6/ptcdata/1/pubpna/US10C_PUBCOMB.seq:*

19: /cgn2_6/ptcdata/1/pubpna/US10C_PUBCOMB.seq:*

19: /cgn2_6/ptcdata/1/pubpna/US10C_PUBCOMB.seq:*

19: /cgn2_6/ptcdata/1/pubpna/US10C_PUBCOMB.seq:*

19: /cgn2_6/ptcdata/1/pubpna/US10C_PUBCOMB.seq:*
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                                    US-10-046-955-7

US-10-046-955-7

US-10-046-955-6

US-09-961-755A-6

US-09-961-755A-8

US-09-961-755A-7

US-09-961-755A-7

US-09-961-755A-7

US-09-961-755A-7

US-09-961-755A-7

US-10-027-632-229494

US-10-027-632-229494

US-10-424-599-66950

US-10-437-963-88990

US-10-437-963-88990
                                    Sequence 59, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 229494,
Sequence 229494,
Sequence 28949,
Sequence 88910, A
Sequence 82910, A
Sequence 82910, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dise APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dise APPLICANT: Morrison, Christine J.

APPLICANT: Morrison, Christine J.

APPLICANT: Reiss, Errol

APPLICANT: Addorevich, Lilana

APPLICANT: Choi, Jong Soo

ITILE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and

TITLE OF INVENTION: Other Filamentous Fungi

FILE REFERENCE: 6395-6206-04

PRICE REPLICATION NUMBER: US/10/046,955

CURRENT APPLICATION NUMBER: US 09/423,233

PRICE APPLICATION NUMBER: US 09/423,233

PRICE APPLICATION NUMBER: PCT/US98/08926

PRICE APPLICATION NUMBER: US 09/423,233

PRICE FILING DATE: 1998-05-01

PRICE APPLICATION NUMBER: US 09/423,200

PRICE APPLICATION PRICE US 09/423,200

PRICE APPLIC
                                        S
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US-10-046-955-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 59, Application US/10046955
; Publication No. US20030129600A1
                                                                                                         Query Match
Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Fusarium
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1 CCCAACTTCTGAATGTTG
                                                                                                                                             Similarity
                                                                                                                Conservative
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ALIGNMENTS

Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB Maximum DB

seq

length:

2000000000

1582 1582 1599 1599 3640 23640 46030 59213 99119 188794 2111 211 211 211 250 350 350

Sequence 12302, A
Sequence 19067, A
Sequence 1249, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 295, App
Sequence 212, App
Sequence 31208, A
Sequence 33208, A
Sequence 33208, A
Sequence 55973, A
Sequence 55973, A
Sequence 9757, Ap
Sequence 9757, Ap
Sequence 47112, A

.6 US-10-242-515-3660 .7 US-10-316-242-11 .3 US-10-424-599-120953 .5 US-10-424-599-120953 .5 US-10-424-599-77094 .3 US-10-027-632-94609 .6 US-10-027-632-305503 .6 US-10-027-632-305503 .6 US-10-027-632-305503 .7 US-10-198-846-3976 .8 US-10-198-846-3976 .9 US-10-369-493-27992 .3 US-10-369-493-27992 .3 US-10-369-114901 .3 US-10-369-1120 .3 US-10-242-535A-33208 .3 US-10-242-535A-5973 .3 US-10-242-535A-5973 .3 US-10-242-535A-59757 .5 US-10-242-535A-9757

Sequence Sequence

4529, Ap 27922, A 114901,

Sequence 94609, A
Sequence 305503,
Sequence 94609, A
Sequence 305503,
Sequence 24598, A
Sequence 24598, A
Sequence 4529, Ap
Sequence 27922, Ap
Sequence 114901,

Total number of hits satisfying chosen parameters:

3340653 seqs, 2534783454 residues

Title: Perfect score:

US-10-046-955-59 18

cccaacttctgaatgttg

OM nucleic - nucleic search, using sw model

Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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October 1,

Scoring table: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

Result

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18 : 319 : 319 : 521 : 522 : 522 : 534 : 666 : 666 : 666 : 382 : 382 : 382 : 382 : 382 : 38444

15 15 15 15 15 15 15 15 15 16 16 17 17 17

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100.0%; Score 18; DB 15; 100.0%; Pred. No. 12;

Length 18

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Gaps

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Mismatches

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; SEQ ID NO 6; LENGTH: 319; TYPE: DNA; ORGANISM: Fusarium solani US-10-046-955-6
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US-10-046-955-6
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CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 7
LENGTH: 310
TYPE: DNA
ORGANISM: Fusarium moniliforme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/10046955
Publication No. US20030129600A1
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                        PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: The Government of the United States of America, as Represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for DivapplicaNT: Control and prevention APPLICANT: Morrison, Christine J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The Government of the United States of APPLICANT: Secretary of the Department of Health APPLICANT: Control and Prevention
                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Aidorevich, Liliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species
TITLE OF INVENTION: Other Filamentous Fungi
                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 6395-62064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 100.0%; Score 18; DB Local Similarity 100.0%; Pred. No. 19; es 18; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Control and Prevention Morrison, Christine J. Reiss, Errol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reiss, Errol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 310;
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RESULT 6 US-09-961-755A-8

Sequence 8, Application US/09961755A Publication No. US20030113722A1 GENERAL INFORMATION:

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                                                                                                                          ; TYPE: DNA
; ORGANISM: Fusarium subglutinans
US-09-961-755A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 60055
CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 521
                                                                                                                                                                                                                                                                               Sequence 5, Application US/09961755A

Publication No. US20030113722A1

GENERAL INFORMATION:

APPLICANT: Beck, Jim

APPLICANT: Barnett, Jason

TITLE OF INVENTION: Detection of Fusarium Species infecting Corn

TITLE OF INVENTION: Polymerase Chain Reaction
                                                                                                                                                                       SOFTWARE: PatentIn version 3.0 SEQ ID NO 5 LENGTH: 522
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Publication No. US20030113722A1
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Best Local
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CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Beck, Jim
APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
TITLE OF INVENTION: Polymerase Chain Reaction
                                                                                                                                                                                                                                                                       FILE REFERENCE: 60055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Gibberella zeae
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 474 CCCAACTTCTGAATGTTG 491
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                               1 CCCAACTTCTGAATGTTG 18
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                                                                            100.0%; Score 18; DE 100.0%; Pred. No. 21;
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APPLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,318
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US-10-027-632-229494/c
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US-09-961-755A-7
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LENGTH: 534
TYPE: DNA
ORGANISM: Fusarium proliferatum
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Matches
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Best Local Similarity
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TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 6005
CURRENT APPLICATION NUMBER: US/09/961,755A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 24
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APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
TITLE OF INVENTION: Polymerase Chain Reaction
FILE REFERENCE: 60055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 522

TYPE: DNA

ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
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100.0%; Pred. No. 21;
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100.0%; Pred. No. 21;
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US-10-027-632-229494
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                                                                     Matches
                                                                                                      Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
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                                                                                                                                                   LOCATION: (1)...(666)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cabou Yihua
APPLICANT: Cabou Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Assorting of Invention: Soy Nucleic Acid Molecules and Other Molecules Assorting Office of Invention: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 66950
LENGTH: 382
TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                             US-10-437-963-82909/c
                                                                                                                                                                                                   RESULT 12
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Publication No. US20040172684A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 4881
LENGTH: 879
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                                                                                                                  Sequence 82909, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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                                    APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Sorghum bicolor
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OTHER INFORMATION: Clone ID: PAT_MRT3847_31471C.1
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Wu, Wei
Boukharov, Andrey A.
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94.4%;
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Pred. No. 1.
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Pred. No. 1.
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1.4e+02;
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Sequence 82910, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC005
                                                                    ; Sequence 3660, Application ; Patent No. US20020147140A1
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                                                                                                                US-09-764-877-3660
                                                                                                                                 RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_82292C.1 US-10-437-963-82909
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 82909
LENGTH: 906
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LENGTH: 1566
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Best Local :
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Best Local Similarity
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FACATION NUMBER: US/10/437,963
CURRENT FAPPLICATION NUMBER: US/10/437,963
CURRENT FILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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LOCATION: (1)..(906)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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Pred. No. 1.7e+02;
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Pred. No. 1
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L.8e+02;
                     and Antibodies
                                                                                                                                                                                                                                                                                                       Length 1566;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005C1
CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,877
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/190,628
PRIOR FILING DATE: 2000-01-31
PRIOR PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/217,487
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3660
LENGTH: 13444
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-3660
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US-10-242-515-3660
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Search completed: October Job time : 75.304 Becs
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PRIOR FILLING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILLING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILLING DATE: 2000-07-11
PRIOR FILLING DATE: 2000-08-14
PRIOR FILLING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILLING DATE: 2000-07-14
                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3660
SEQ ID NO 3640
LENGTH: 13444
TYPE: DNA
ORGANIUM: Homo sapiens
S-10-242-515-3660
                                                                                                                                                                               Query Match 91.1
Best Local Similarity 94.4
Matches 17; Conservative
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Best Local S
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Local Similarity 94.4%; Pred. No. 2.7e+02;
hes 17; Conservative 0; Mismatches 1;
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Maximum Match 100%
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CG037213
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AQ365757
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CU9910198
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BII11174
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BJ108367
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CEO70578 tigr-gssAW857322 CM1-CT030
BY726648 BY726648
AW861372 CM1-CT030
CA188988 SCCCCL4C0
CB657614 OSJNEC138
BY739516 BY739516
AV382703 AV382703
CB657615 OSJNEC138
BZ995379 PUFID06TB
BZ995379 PUFID06TB
BZ995379 PUFID6TB
BU417573 603232992
CC382957 PUHNG88TD
CG165155 PUJEL74TB
BZ165155 PUJEL74TB
BZ16939 CH230-44C
BM919869 AGENCOURT

CD885707
BJ108357
CE323958
AQ665757
CA032813
BJ126336
CD910198
AW857324
CA220452
AW857329
CE070578
AW857329
CE070578

7 G118.100C 7 BJ108367 8 Ligr-g88-1 HS 5354 B 1 HX14E137 8 HX126336 8 J126336 8 G468.114K 1 CM1-CT030 8 CSBFIL01 1 602899366 CM1-CT030

AV214144 AV214144
AV109406 AV109406
AQ204622 HS 3329 B
BJ590299 BJ590299
B1396526 r054all.y
CC843236 NDL.112C2
CB824672 r229f02.y
CB376989 rq16d06.y
CB376988 rq44b02.y
BX469546 BX469546
CB564460 AGENCOURT
CG122910 PUFUJ67TB

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 379)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,

Le,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,

Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Parange,C., Rifkin,L.,

Mardis,E., Moore,B., Morris,M., Parange,C., Rifkin,L.,

Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,

Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,

and Marra,M. 8889549 Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996) 97044478 AA112191 379 bp mRNA linear EST 01-AUG-ZDEGOEO2.rl Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562586 5' similar to WP:F08C6.3 CE02592 ;, mRNA sequence. AA112191 EST 01-AUG-1997

Result No.

Score

Query Match

Length

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AA112191 W19631 BE592535 BU713295

AA112191 zn60e02.r W19631 zb35d09.r1 BE592535 WS1_94_C1 BU713295 SJAABOB11

COMMENT

Louis,

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TITLE
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17; Conserva
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High quality sequence stop: 287.
Location/Qualifiers
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Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 768 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           403 bp
zb35d09.rl Soares parathyroid tu
IMAGE:305585 5', mRNA sequence.
W19631
                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Barkway, Box 8501, St. 1 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                   Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 403)
                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W19631.1 GI:1295540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domo sapiens (human)
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                                                                                                                          quality sequence stop: 264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene muscle 937209"
/clone_lib="Stratagene muscle; Vector: pBluescript SK-;
/note="Torgan: skeletal muscle; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally.
Primer: Oligo dT. Skeletal muscle from pattent with
malignant hyperthermia. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:4595876"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="muscle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:562586"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1248995"
/db_xref="taxon:9606"
                                                                                                        ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DB 9; Pred. No. 2.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   op mRNA line
_tumor_NbHPA Homo
                                                                                                                                                                                                                                                                             St. Louis, MO 63108
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cDNA clone
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VERSION
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BE592535
                                                                                                                                                                                                                                                                FEATURES
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE592535
BE592535.1 GI:9847608
EST.
                                                                                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukāryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 473)
                                                                                                                                                                                                                                                                                                                                         Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE592535 473 bp mRNA linear EST 18-AUG-2000
WS1_94_C12.b1_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
                                                                                                                                                                                                                                                                                           POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An EST database from Sorghum: water-stressed plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pratt,L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sorghum bicolor (sorghum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAACTTATGAATGTTG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCAACTTCTGAATGTTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
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                                                                                                                                                                                                                                                                                                                quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db xref="taxon:4558"
/db xref="taxon:4558"
/clone lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site_1: XhOI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAp II. Clones to be sequenced were prepared by mass excision."
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/dev_stage="adult"
/lab host="DH10B (ampicillin resistant)"
/clone_lib="Soares parathyroid tumor_NbHPA"
/clone_Tib="Soares parathyroid gland; Vector: pT7T3D
/note="Organ: parathyroid gland; Vector: pT7T3D
(pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed wIth a Not I
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                          .473
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94.4%;
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BU713295
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MEDLINE
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Best Local
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Hu, W., Yan, O., Shen, D.K., Liu, F., Zhu, Z.D., Song, H.D., Xu, X.R., Wang, Z.J., Rong, Y.P., Zeng, L.C., Wu, J., Zhang, X., Wang, J.J., Xu, X.N., Wang, S.Y., Fu, G., Zhang, X.L., Wang, Z.Q., Brindley, P.J., Xu, X.N., Wang, S.Y., Fu, G., Zhang, X.L., Wang, Z.Q., Brindley, P.J., McManus, D.P., Xue, C.L., Feng, Z., Chen, Z. and Han, Z.G.

Byolutionary and biomedical implications of a Schistosoma japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schistosoma japonicum
Schistosoma japonicum
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
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BU713295.1 GI:28320657
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SJAABOB11 Adult SjC 7/94
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                                                                                  /clone lib="Moult Sig 7/94"
//clone lib="Moult Sig 7/94"
//note="Wector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2: Xhol I; Several hundred adult Schistosoma japonicum (Anhui, P.R. China, strain), of mixed sex, were perfused from the mesenteries of experimentally infected mice and rabbits at the Queensland Institute of Medical Research, Brisbane, Australia (QIMR), and stored for several months in liquid nitrogen. Subsequently, mRNA was isolated at the QIMR from lysates of these worms by oligo dT chromatography, using a kit from Pharmacia. The mRNA was then shipped to Clontech, Palo Alto, CA, USA, who constructed a cDNA library. First strand synthesis was primed with an oligo-dT-Xhol-grimer and synthesis was primed with an oligo-dT-Xhol-grimer and synthesis was accomplished with RNAse H and T4 DNA polymerase. The double stranded cDNA was ligated to EcoRI linkers, digested with EcoRI and XhoI, and ligated into the phagemid vector lambda ZAP II XR. After construction of this directional library by Clontech, it was returned to the QIMR. During analysis of the library at the QIMR, we have found that a small percentage, 2% to 3%, of the clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by hybridization analysis to genomic DNA from salmon (Sigma hybridization salmon (Sigma hybridization analysis to genomic DNA from salmon (Sigma hybridization salmon (Sigma hybridization salmon (Sigma hybridization salmon (Sigma hybridization salmon (Sigma Sigma Hybridization salmon (Sigma Sigma Sigma
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Location/Qualifiers
hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male and female"
/tissue_type="Whole body"
/dev_stage="Adult worms"
/lab_host="Mouse and rabbit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Schistosoma japonicum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain="Chinese (Anhui)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:6182"
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94.4%;
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Pred. No. 2.2e+03;
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Schistosoma japonicum cDNA,
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                                         Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
Rhabditoidea; Rhabditidae; Pel
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Triticum aestivum (bread wheat)
Triticum aestivum
Vividiolantae; Strep
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17; Conser
1 (bases 1 to 548)
Kohara, Y., Shin-i, T.,
and Sugano, S.
                                                                                                     BJ108367.2
EST.
                                                                                                                                              BJ108367 unpublished of Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                             Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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                                                                                       Caenorhabditis elegans
                                                                                                                                   BJ108367
                                                                                                                                                                             BJ108367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoplante.
Genoplante, a major partnership french
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (bases 1 to 524)
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                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="grain
pollination)"
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/cultivar="recital"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                     clone_lib="G118"
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               Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y
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Pred. No. 2.3e+03;
0; Mismatches 1
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Pred. No. 2.3e+03;
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                                            la; Chromadorea; Rhabditida;
Peloderinae; Caenorhabditis
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cDNA library, C. elegans
yk1107all 5', mRNA sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tigr-gss-dog-17000360306070 D genomic survey sequence.
                                                                                                                                                                                                                                                                 The Institute for Genomic Research Department of Eukaryotic Genomics, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; 1 (bases 1 to 555)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remi Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C. Venter; J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A complementary view of the C.elegans genome Unpublished (2002)
On Jan 23, 2002 this sequence version replaced gi:18268395.
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                      14512627
                                                                                                                                                                                                                                                                                                                                                                   The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CE323958.1 GI:36133381
                                                                                                                                                                                                                    Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                      Contact: Kirkness EF
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Location/Qualifiers
                                                  peripheral
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elegans L1 stage"
                                                  /clone lib="Dog Library"
/note="Site 1: BstXI; Libraries were
peripheral blood"
                                                                                               /mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
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/clone_lib="unpu
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/tissue_type="whole animal"
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/clone="yk1107a11"
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                                                                                                                                     organism="Canis familiaris"
/mol_type="genomic DNA"
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HS_5354_B2_E01_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic_clone Plate=930 Col=2 Row=J, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 579)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ665757.1 GI:5173525 GSS.
                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 579.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: T7
Class: BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.htsc.washington.edu
Plate: 930 row: J column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Pax: (206) 615-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                            Similarity
                                     CCCAACTTCTGAATGTTG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                     .āss: BAC ends
                                                                          Conservative
                                                                                                                                                                                  /clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen do
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
                                                                                                                                                                      pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                1. .579
                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                    clone="Plate=930 Col=2 Row=J"
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 443
                                                                          Score 16.4; Di
Pred. No. 2.4e
0; Mismatches
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RESULT 9 CA032813/c

Locus

CA032813

584 bp

mRNA

linear

EST 24-OCT-2002

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RESULT 10
BJ126336/c
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                                                                                          Caenorhabditis elegans
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Eukaryota; - hahditidae: Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                           BJ126336 unpublished oligo-capped cDNA library, C. elegans L1 Caenorhabditis elegans cDNA clone ykl333h08 5', mRNA sequence. BJ126336
                                      1 (bases 1 to 587)
Kohara,Y., Shin-i,T., Thierry-Mieg,J.,
and Sugano,S.
A complementary view of the 
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: stein@ipk-gatersleben.de
Insert Length: 584 Std Error:
Plate: 14 row: E column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 584)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and
EST sequencing and analysis in barley (2002)
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vulgare subsp. vulgare Hordeum vulgare subsp. vulgare
                                                                                                                                                                                                          BJ126336.1 GI:18286488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Stein Nils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5-PRIME, mRNA sequence
CA032813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 039482-5595
                                                                                                                                                                                                                                                                                                                                                                                                                      CCCAACTTCTGAATGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI,PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="apex"
/dev_stage="apex (3-5 mm
/lab_host="XL10-Gold"
/clone_lib="HX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cultivar="barke"
/sub_species="vulgare"
/db_xref="GABI:273489"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="HX14E13"
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94.4%;
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Pred. No. 2.4e+03;
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                   C.elegans genome
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                                                            Thierry-Mieg, D.,
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                                                            Suzuki,Y.
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17; Conserv
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                                                                                                                                                                                                                                                            Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                       Genoplante.
Genoplante, a major
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum (bread wheat)
Triticum aestivum
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EST.
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                        Contact: Genoplante
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tadasu Shin-i
                                                          Similarity
CCCAACTTCTGAATGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 604)
                                                                                                                                                                                                                                                                                                                                            rue Henri Rochefort 91025 EVRY CEDEX France
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/dev stage="L1"
/clone_lib="unpublished oligo-capped cDNA library,
elegans L1 stage"
                                                                                                                  /tissue_type="grain
pollination)"
/clone_lib="G468"
                                                                                                                                                               'db_xref="taxon:4565"
'clone="G468114K19"
                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="recital"
                                                                                                                                                                                                                         organism="Triticum aestivum"
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/strain="N2"
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                                            Score 16.4; DB 14
Pred. No. 2.4e+03;
0; Mismatches 1
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Pred. No. 2.4e+03
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                                                                       Length 604;
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AW857324/c
ACCESSION
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KEYWORDS
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CA220452
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(bases 1 to 606)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Coldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., GeOliveira, P.S., Buukuma, A., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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CM1-CT0309-071299-057-b10
                                                                                                                                                                                                                                                                                                          l Similarity
17; Conser
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM1-CT0309-071
299-057-b10&t3=1999-12-07&t4=1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                      5', mRNA sequence.
CA220452
CA220452.1 GI:352
                                                                                     SCSBFL4014F10.g FL4 Saccharum
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="CT0309"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: Note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                               stringency conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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94.4%;
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Pred. No. 2.4e+03;
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) CT0309 Homo sapiens cDNA,
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphr
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clade; Panicoideae; Andropogoneae; Sac

1 (bases 1 to 616)

Vettore,A.L., da Silva,F.R., Kemper,E.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br Plate: 014 row: F column: 10 Seq primer: T7 Promoter Primer.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 55 19 3788 1137 Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
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                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 631)
                                                                                                                                                                                                                                                                                                                                                                                  BI111174
BI111174.1 GI:14562075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: parruda@unicamp.br
                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                               Mus musculus
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//note="Organ: Developed inflorescence and rachis
//note="Organ: Developed inflorescence and rachis
(20cm-long); Vector: pSportl; Site 1: SalI; Site 2: NotI;
(20cm-long); Vector: pSportl; Site 1: GalI; Site 2: NotI;
(20cm-long); CoNA was prepared inflorescence and rachis (20cm-long)]. CDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sixing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCSBFL4014F10"
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Pred. No. 2.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp mRNA linear EST 26-JUN-2001 musculus cDNA clone IMAGE:5029192 5',
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                                                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=CM1-CT0309-071
299-057-gl1&t3=1999-12-07&t4=1)
                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 632)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW857329 632 bp mRNA linear EST 19-MAY-200 CM1-CT0309-071299-057-gl1 CT0309 Homo sapiens cDNA, mRNA sequence. AW857329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW857329.1 GI:7953022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCAACTTCAGAATGTTG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAACTTCTGAATGTTG 18
                                                                   primer: puc 18 forward
h quality sequence stop: 630.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop:
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=Torgan: mammary; Vector: pCMV-SPORT6; Site 1: Sali
Site 2: Not1; Cloned unidirectionally. Primer: Ōligo di
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'strain="C57BL/6J"
                                                    . 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DB 12;
Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                     01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 19-MAY-2000
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/db_xref="taxon:9606"
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/clone_lib="CT0309"
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ORIGIN

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Best Local Similarity
Matches 17; Conserv
                      Query Match
 Conservative
        91.1%;
Score 16.4; DB 10
Pred. No. 2.4e+03;
0; Mismatches 1
                     DB 10;
 Indels
                    Length
0
 Gaps
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